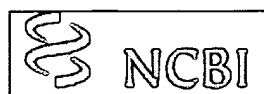
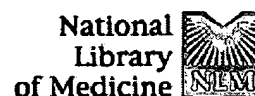


09/622,613
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- Search History will be lost after eight hours of inactivity.
- To combine searches use # before search number, e.g., #2 AND #6.
- Search numbers may not be continuous; all searches are represented.

Search	Most Recent Queries	Time	Result
#2	Search rana pipiens AND ribonuclease	15:20:36	<u>35</u>
#1	Search rana pipiens	15:16:35	<u>5676</u>

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Jan 20 2004 07:12:30

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us-protein - protein search, using sw model

Run on: January 22, 2004, 12:01:21 ; Search time 25.7079 Seconds
(without alignments)
1043.940 Million cell updates/sec

Title: US-09-622-613C-2
Perfect score: 578
Sequence: 1 QDWLTFQKHLTNTTRDVCN.....TFCVTCENQAPVAFVGVGHC 104

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 830525 seqs, 258052604 residues
Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SP archaea:*
2: SP bacteria:*
3: SP fungi:*
4: SP human:*
5: SP invertebrate:*
6: SP mammal:*
7: SP mhc:*
8: SP organelle:*
9: SP phage:*
10: SP plant:*
11: SP rodent:*
12: SP virus:*
13: SP vertebrate:*
14: SP unclassified:*
15: SP virus:*
16: SP bacteriophage:*
17: SP archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	578	100.0	127	13	Q918V8
2	556	96.2	127	13	Q8UYX5
3	404.5	70.0	129	13	Q9DFY6
4	386	66.8	128	13	Q9DFY8
5	311	53.8	128	13	Q9DFY7
6	309	53.5	128	13	Q9DFY5
7	298	51.6	133	13	Q98SMO
8	292	50.5	133	13	Q9PMR7
9	286	49.5	133	13	Q98SL9
10	285	49.3	132	13	Q98SM2
11	282	48.8	133	13	Q98SL8
12	280	48.4	132	13	Q98SM1
13	275.5	47.7	132	13	Q9DF78
14	257.5	27.2	169	13	Q9W738
15	129	22.3	152	11	Q9JK15
16	127	22.0	157	11	Q9JK19

17	126.5	21.9	153	11	Q9JK17	Q9JK17 mus saxicol
18	126	21.8	157	11	Q9JK3	Q9JK3 meriones un
19	125	21.6	157	11	Q9JK4	Q9JK4 meriones un
20	123	21.3	154	11	Q9JK8	Q9JK8 mus saxicol
21	122	21.1	157	11	Q9JK1	Q9JK1 meriones un
22	121	20.9	157	11	Q9JK2	Q9JK2 meriones un
23	120.5	20.8	155	11	Q9JK9	Q9JK9 mus pahari
24	119.5	20.7	155	11	Q9JK3	Q9JK3 mus saxicol
25	116.5	20.2	155	11	Q9JK6	Q9JK6 mus saxicol
26	115.5	20.0	132	6	Q9TV25	Q9TV25 eulimur ful
27	115.5	20.0	155	11	Q9JK12	Q9JK12 mus saxicol
28	115.5	20.0	155	11	Q9JK14	Q9JK14 mus saxicol
29	114.5	19.8	170	6	Q9BECL	Q9BECL tragulus ja
30	113.5	19.6	119	6	Q9TSC6	Q9TSC6 cercopithec
31	113.5	19.6	119	6	Q9TV32	Q9TV32 gorilla gor
32	113.5	19.6	132	6	Q9TV24	Q9TV24 galago moho
33	113.5	19.6	147	6	Q9H200	Q9H200 pan troglod
34	113.5	19.6	155	11	Q9R134	Q9R134 tatus nov
35	113	19.6	156	11	Q9JK6	Q9JK6 mus caroli
36	113	19.6	156	11	Q9JK7	Q9JK7 mus caroli
37	112.5	19.5	119	6	Q9TV30	Q9TV30 saginus oe
38	112.5	19.5	155	11	Q9R125	Q9R125 mus musculu
39	112.5	19.5	155	11	Q9JK8	Q9JK8 mus pahari
40	112	19.4	124	6	Q9TSP2	Q9TSP2 bos taurus
41	112	19.4	156	11	Q9JK7	Q9JK7 mus caroli
42	111.5	19.3	155	11	Q9JK3	Q9JK3 mus caroli
43	111	19.2	124	6	Q9SNE6	Q9SNE6 bubalus bub
44	111	19.2	156	6	Q8SQ04	Q8SQ04 lemur catra
45	111	19.2	156	11	Q9JK4	Q9JK4 mus caroli

ALIGNMENTS

RESULT 1

Q918V8 PRELIMINARY; PRT; 127 AA.
AC Q918V8;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Oncogene variant rapRL precursor.
OS Rana pipiens (Northern leopard frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8404;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA MEDLINE=20330357; PubMed=10871370;
RA Chen S.-L., Le S.-Y., Newton D.L., Maizel J.V., Jr., Rybak S.M.;
RT "A gender-specific mRNA encoding a cytoxic ribonuclease contains a
RT 3' UTR of unusual length and structure."
BL Nucleic Acids Res. 28:2375-2382(2000).
DR EMBL; AF165133; AAF76935.1; -.
DR HSSP; P22069; IONC.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; RNaseA.1.
DR ProDom; PD000535; RNaseA.1.
DR SMART; SM00092; RNase_Pc.1.
DR PROSITE; PS00127; RNASE_PANCREATIC.1.
KW SIGNAL.
FT SIGNAL. 1 23 POTENTIAL.
SQ SEQUENCE 127 AA; 14491 MW; B8511DC5407AB69B CRC64;

Query Match 100.0%; Score 578; DB 13; Length 127;

Best Local Similarity 100.0%; Pred. No. 4.3e-58; Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QDWLTFQKHLTNTTRDVCNIMSTNLFCHKDKNTFIYSRPPVRAICGIIASXVLT 60
Db 24 QDWLTFQKHLTNTTRDVCNIMSTNLFCHKDKNTFIYSRPPVRAICGIIASXVLT 83

QY 61 SEFYLSDCNVTSRPCKYKLLKKSNTFCVTCENQAPVHFGVGHG 104
DB 84 SEFYLSDCNVTSRPCKYKLLKKSNTFCVTCENQAPVHFGVGHG 127

RESULT 2

Q8UVX5 PRELIMINARY; PRT; 127 AA.

AC Q8UVX5; 08UVX5; 01-MAR-2002 (Tremblrel. 20, Created)

DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)

DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)

DE Oncoprase precursor.

GN RPR.

OS Rana pipiens (Northern leopard frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.

OX NCBI_TaxID=8404;

RM [1]

RP SEQUENCE FROM N.A.

RA Liao Y.-D., Wang S.-C.;

RT "Rana pipiens oncoprase genomic DNA";

RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF332139; AAL54383.1; -

DR InterPro; IPR001427; RNaseA.

DR Pfam; PF00074; RNaseA; 1.

DR ProDom; PD000535; RNaseA; 1.

DR SMART; SM00092; RNase_Pc; 1.

DR PROSITE; PS00127; RNASE_PANCREATIC; 1.

KM Signal.

FT SIGNAL. 1 23 POTENTIAL.

SQ SEQUENCE 127 AA; 14469 MW; 953F90D31CEE3F CRC64;

Query Match 96.2%; Score 556; DB 13; Length 127;

Best Local Similarity 96.2%; Pred. No. 1.4e-55;

Matches 100; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 QDWLTFOKGLTNRDVDCNNIMSTNLFHCKDKNTFYISRPVPAKICGIIASKVLT 60

DB 24 QDWLTFOKGLTNRDVDCNNIMSTNLFHCKDKNTFYISRPVPAKICGIIASKVLT 83

QY 61 SEFYLSDCNVTSRPCKYKLLKKSNTFCVTCENQAPVHFGVGHG 104

DB 84 SEFYLSDCNVTSRPCKYKLLKKSNTFCVTCENQAPVHFGVGHG 127

RESULT 3

Q9DFY6 PRELIMINARY; PRT; 129 AA.

AC Q9DFY6; 09DFY6; 01-MAR-2001 (Tremblrel. 16, Created)

DT 01-OCT-2001 (Tremblrel. 18, Last sequence update)

DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)

DE RC-RNase4 ribonuclease precursor.

OS Rana catesbeiana (Bull frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.

OX NCBI_TaxID=8400;

RM [1]

RP SEQUENCE FROM N.A.

RA MEDLINE=20512555; PubMed=11058105;

RT "Purification and cloning of cytoxic ribonucleases from Rana

catesbeiana (bullfrog)";

RL Nucleic Acids Res. 28:4097-4104 (2000).

RM [2]

RP SEQUENCE FROM N.A.

RA TISSUE=Liver;

RT Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.

EMBL; AF242555; AAG31441.2; -

HS99; P22069; IONC.

Q9DFY6

Q9DFY7

DR InterPro; IPR001427; RNaseA.

DR Pfam; PF00074; RNaseA; 1.

DR ProDom; PD000535; RNaseA; 1.

DR PROSITE; PS00127; RNASE_PANCREATIC; 1.

KM Signal.

FT SIGNAL. 1 23 POTENTIAL.

FT CHAIN 24 129 RC-RNASE4 RIBONUCLEASE.

SQ SEQUENCE 129 AA; 14724 MW; 826A628B2B10ABDA CRC64;

Query Match 70.0%; Score 404.5; DB 13; Length 129;

Best Local Similarity 67.6%; Pred. No. 2.5e-38;

Matches 71; Conservative 16; Mismatches 17; Indels 1; Gaps 1;

QY 1 QDWLTFOKGLTNRDVDCNNIMSTNLFHCKDKNTFYISRPVPAKICGIIASKVLT 60

DB 24 QDWLTFOKGLTNRDVDCNNIMSTNLFHCKDKNTFYISRPVPAKICGIIASKVLT 83

QY 61 SEFYLSDCNVTSRPCKYKLLKKSNTFCVTCENQAPVHFGVGHG 104

DB 84 SEFYLSDCNVTSRPCKYKLLKKSNTFCVTCENQAPVHFGVGHG 128

RESULT 4

Q9DFY8 PRELIMINARY; PRT; 128 AA.

AC Q9DFY8; 09DFY8; 01-MAR-2001 (Tremblrel. 16, Created)

DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)

DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)

DE RC-RNase2 ribonuclease precursor.

OS Rana catesbeiana (Bull frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.

OX NCBI_TaxID=400;

RM [1]

RP SEQUENCE FROM N.A.

RA TISSUE=Liver;

RT Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF242553; AAG31439.1; -

DR HSSP; P22069; IONC.

DR InterPro; IPR001427; RNaseA.

DR Pfam; PF00074; RNaseA; 1.

DR ProDom; PD000535; RNaseA; 1.

DR PROSITE; PS00127; RNASE_PANCREATIC; 1.

KM Signal.

FT SIGNAL. 1 23 POTENTIAL.

FT CHAIN 24 128 RC-RNASE2 RIBONUCLEASE.

SQ SEQUENCE 128 AA; 14839 MW; 989719CF52053CC CRC64;

Query Match 66.8%; Score 386; DB 13; Length 128;

Best Local Similarity 67.3%; Pred. No. 3.1e-36;

Matches 70; Conservative 10; Mismatches 24; Indels 0; Gaps 0;

QY 1 QDWLTFOKGLTNRDVDCNNIMSTNLFHCKDKNTFYISRPVPAKICGIIASKVLT 60

DB 24 QDWLTFOKGLTNRDVDCNNIMSTNLFHCKDKNTFYISRPVPAKICGIIASKVLT 83

QY 61 SEFYLSDCNVTSRPCKYKLLKKSNTFCVTCENQAPVHFGVGHG 104

DB 84 SEFYLSDCNVTSRPCKYKLLKKSNTFCVTCENQAPVHFGVGHG 127

RESULT 5

Q9DFY7

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OM protein - protein search, using sw model

Run on: January 22, 2004, 12:01:20 ; Search time 11.6854 Seconds
(without alignments)
855.901 Million cell updates/sec

Title: US-09-622-613c-2
Perfect score: 578
Sequence: 1 QDWLTFQKHLNTRDVCN.....TFCVTCENQAPVHFVGVGHC 104

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 9616862 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	553	95.7	104	2 A39035	ribonuclease-relat
2	289	50.0	111	2 A27121	ribonuclease-relat
3	285.5	49.4	111	2 JX0120	ribonuclease-relat
4	269.5	46.6	111	2 JX0085	pancreatic ribonuc
5	149	25.8	119	2 S41111	pancreatic ribonuc
6	131	22.7	124	1 NRUI	pancreatic ribonuc
7	128	22.1	125	1 A32474	angiogenin (valida
8	126	21.8	128	1 NRCU	pancreatic ribonuc
9	125	21.6	124	1 NRMHK	pancreatic ribonuc
10	120	20.8	124	1 NRKS	pancreatic ribonuc
11	119.5	20.7	145	1 A35932	pancreatic ribonuc
12	119	20.6	128	1 NRCBP	angiogenin precurs
13	117	20.2	124	1 NRCB	pancreatic ribonuc
14	116	20.1	125	1 B43825	pancreatic ribonuc
15	116	20.1	128	1 NRYV	pancreatic ribonuc
16	114	19.7	124	1 NRHP	pancreatic ribonuc
17	113	19.6	127	1 NRHDUG	angiogenin precurs
18	112	19.4	124	1 NRBOB	pancreatic ribonuc
19	112	19.4	124	1 NRPG	pancreatic ribonuc
20	112	19.4	150	1 NRBO	pancreatic ribonuc
21	111.5	19.3	147	2 I52489	ribonuclease 4 (EC
22	111	19.2	124	2 S08549	ribonuclease - dom
23	111	19.2	128	1 NRHO	pancreatic ribonuc
24	111	19.2	128	1 NRPO	pancreatic ribonuc
25	110.5	19.1	167	2 S20066	pancreatic ribonuc
26	110.5	19.1	123	1 A43825	pancreatic-type ri
27	110.5	19.1	155	2 JG6159	angiogenin - pig
28	109	18.9	124	1 NRSH	eosinophil-associa
29	109	18.9	124	1 NRPH	pancreatic ribonuc

30	109	18.9	124	1 NRGA	pancreatic ribonuc
31	109	18.9	124	1 S07141	pancreatic ribonuc
32	108	18.7	124	1 NRMB	pancreatic ribonuc
33	108	18.7	124	1 NRGN	pancreatic ribonuc
34	107	18.5	124	1 NRGF	pancreatic ribonuc
35	106	18.3	156	2 JG6160	eosinophil-associa
36	105	18.2	124	1 NRDEO	pancreatic ribonuc
37	105	18.2	124	1 NRDM	pancreatic ribonuc
38	105	18.2	124	1 NRDM	pancreatic ribonuc
39	105	18.2	124	1 NRDM	pancreatic ribonuc
40	105	18.2	124	1 NRDM	pancreatic ribonuc
41	104	18.0	124	1 NRHY	pancreatic ribonuc
42	103	17.8	124	1 NRDER	pancreatic ribonuc
43	103	17.8	124	1 NRDN	pancreatic ribonuc
44	103	17.8	124	1 NRKN	pancreatic ribonuc
45	102	17.6	124	1 NRDEP	pancreatic ribonuc

ALIGNMENTS

RESULT 1
A39035
ribonuclease-related anti-tumor protein - northern leopard frog (fragment)
C/Species: Rana pipiens (northern leopard frog)
C/Date: 31-Jul-1991 #sequence_revision 31-Jul-1991 #text_change 30-Jun-1993
C/Accession: A39035
R/Ardele, W.; Mikulski, S.M.; Shogen, K.
J. Biol. Chem. 266, 245-251, 1991
A/Title: Amino acid sequence of an anti-tumor protein from Rana pipiens oocytes and early
A/Reference number: A39035; MUID:91093131; PMID:1985896
A/Accession: A39035
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-104 <ARD>
C/Superfamily: pancreatic ribonuclease

Query Match 95.7%; Score 553; DB 2; Length 104;
Best Local Similarity 95.2%; Pred. No. 1.1e-48;
Matches 99; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 QDWLTFQKHLNTRDVCNINMSTNLFHCKDKKTFIYSRPEPVKAICKGIASKNVLT 60
DB 1 EDWLTFQKHLNTRDVCNINMSTNLFHCKDKKTFIYSRPEPVKAICKGIASKNVLT 60
QY 61 SEFYLSDCNVTSRPCYKLLKKSNTFCVTCENQAPVHFVGVGHC 104
DB 61 SEFYLSDCNVTSRPCYKLLKKSNTFCVTCENQAPVHFVGVGSC 104

RESULT 2

A27121
ribonuclease-related sialic acid-binding lectin - bullfrog
C/Species: Rana catesbeiana (bullfrog)
C/Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 30-Jun-1993
C/Accession: A27121
R/Titani, K.; Takio, K.; Kuwada, M.; Nitta, K.; Sakakibara, F.; Kawachi, H.; Takayanagi, Biochemistry 26, 2189-2194, 1987
A/Title: Amino acid sequence of sialic acid-binding lectin from frog (Rana catesbeiana)
A/Reference number: A27121; MUID:8729649; PMID:3304421
A/Molecule type: protein
A/Residues: 1-111 <RTT>
C/Superfamily: pancreatic ribonuclease
C/Keywords: lectin

Query Match 50.0%; Score 289; DB 2; Length 111;
Best Local Similarity 48.6%; Pred. No. 4.2e-22;
Matches 54; Conservative 17; Mismatches 32; Indels 8; Gaps 3;

QY 1 QDWLTFQKHLNTRDVCNINMSTNLFHCKDKKTFIYSRPEPVKAICKGIASKN 56
DB 1 ENWATFOQKHIIINTPIINCNTIMDNNIYIVGCGCKXVNFPIISATTVKACIGVLI-MNN 59

R:Bond, M.D.; Strydom, D.J. Biochemistry 28, 6110-6113, 1989
A>Title: Amino acid sequence of bovine angiotensin.
A:Reference number: A32474; MUID:89375344; PMID:2775757
A:Accession: A32474
A:Molecule type: protein
A:Residues: 1-125 <BON>
A:Experimental source: plasma
R:Maes, P.; Danart, D.; Pommen, C.; Montreuil, J.; Spik, G.; Tattar, A. FEBS Lett. 241, 41-45, 1988
A>Title: The complete amino acid sequence of bovine milk angiotensin.
A:Reference number: S02001; MUID:89065101; PMID:3197838
A:Accession: S02001
A:Molecule type: protein
A:Residues: 1-125 <MAE>
A:Experimental source: milk
R:Acharya, K.R.; Shapiro, R.; Riordan, J.F.; Vallee, B.L. submitted to the Brookhaven Protein Data Bank, January 1995
A:Reference number: A65065; PDB:1AG1
A:Contents: annotation: X-ray crystallography, 1.5 angstroms, residues 1-125
R:Acharya, K.R.; Shapiro, R.; Riordan, J.F.; Vallee, B.L. Proc. Natl. Acad. Sci. U.S.A. 92, 2949-2953, 1995
A>Title: Crystal structure of bovine angiotensin at 1.5 Angstroms resolution.
A:Reference number: A58315; MUID:95224057; PMID:7708754
A:Contents: annotation: X-ray crystallography, 1.5 angstroms
R:Leguin, O.; Albaret, C.; Bontems, F.; Spik, G.; Lallemand, J.Y. submitted to the Brookhaven Protein Data Bank, April 1996
A:Reference number: A65709; PDB:1G10
A:Contents: annotation: conformation by (1)H-NMR, residues 1-125
R:Leguin, O.; Albaret, C.; Bontems, F.; Spik, G.; Lallemand, J.Y. Biochemistry 35, 8870-8880, 1996
A>Title: Solution structure of bovine angiotensin by (1)H nuclear magnetic resonance spectroscopy.
A:Reference number: A58821; MUID:96280645; PMID:8688423
A:Contents: annotation: conformation by (1)H-NMR
R:Reisdorf, C.; Abergel, D.; Bontems, F.; Lallemand, J.Y.; Decottignies, J.P.; Spik, G. Eur. J. Biochem. 224, 811-822, 1994
A>Title: Proton resonance assignments and secondary structure of bovine angiotensin.
A:Reference number: S48212; MUID:95010071; PMID:7925406
A:Contents: annotation: conformation by (1)H-NMR
A:Function:
C:Description: hydrolyzes tRNA; induces vascularization of normal and malignant tissues
C:Superfamily: pancreatic ribonuclease
C:Keywords: angiogenesis; hydrolase; nucleic acid degradation
F:60-68/Region: receptor binding #status predicted
F:14,41,115/Active site: His, Lys, His #status predicted
F:27-82,40-93,58-108/Disulfide bonds: #status experimental

Query Match 22.1%; Score 128; DB 1; Length 125;
Best Local Similarity 34.0%; Pred. No. 7.66-06;
Matches 33; Conservative 14; Mismatches 32; Indels 18; Gaps 5;

Qy 16 DVDGNNIMTNLF--HCKDKNTFYSPRPYKAIKGIISKN-----VLTTSEFYL 65
Db 24 DEYCFNNMKNNRLTRPCDKRNTFIHGNNDIKALICE---DRNGQPYRGDLRIKSKSFQI 79
Qy 66 SDC---NWTSP-PCKYTKKSTNTFCVTCENQAVHF 98
Db 80 TICNKGSSRPCKRYGATESRVIIVGCEGLPVHF 116

RESULT 8
NRCU
pancreatic ribonuclease (EC 3.1.27.5) - nutria (tentative sequence)
N:Alternate names: RNase 1; RNase A
C:Species: Myocastor coypus (nutria, coypu)
C:Date: 24-Apr-1994 #sequence_revision 30-Sep-1988 #text_change 31-Mar-2000
C:Accession: A00822
R:van den Berg, A.; van den Hende-Timmer, L.; Beintema, J.J. Biochim. Biophys. Acta 453, 400-409, 1976
A>Title: Isolation, properties and primary structure of coypu and chinchilla pancreatic
A:Reference number: A90612; MUID:77065676; PMID:999896
A:Accession: A00822
A:Molecule type: protein

```

A:Residues: 1-128 <VAN>
C:Superfamily: pancreatic ribonuclease
C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F.12/.41.119/Active site: His, Lys, His #status predicted
F./26-.84.40-95.58-110.65-72/Disulfide bonds: #status predicted
F./34/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match      21.8%; Score 126; DB 1; Length 128;
Best Local Similarity 29.9%; Pred. No. 1.2e-05;
Matches 35; Conservative 18; Mismatches 36; Indels 28; Gaps 7;

Oy 6 FOKKIL-----TNTRDVDCNIM-STNLF--HCKDKQTFIYSRDEPKVAKIGIIASKKV 57
    |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 8 PERGMDSNGSSTNNYCNEMMKSRMTGCRKPVTTPHEPLADVAVC----FOKNV 63

Oy 58 I-----TTSEFYLSDCNVTSRP---CKYKLKKSTNTFCVTENO--APVHF 98
    |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 64 LCKNGQTNCYGSNSMHIITDCRVTSNDYPNCISYRTSGEKSIVACGNPVPVPHF 120

RESULT 9
NRWHR
pancreatic ribonuclease (BC 3.1.27.5) - minke whale
N:Alternate names: RNase 1; RNase A
C:Species: Balenoptera acutorostrata (minke whale, lesser rorqual)
C>Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 03-Jun-1994
C:Accession: A00818
R:Eimmens, M.; Welling, G.W.; Beintema, J.J.
Biochem. J. 157, 317-323, 1976
A>Title: The amino acid sequence of pike whale (lesser rorqual) pancreatic ribonuclease.
A:Reference number: A00818; MUID:76277855; PMID:962870
A:Accession: A00818
A:Molecule type: protein
A:Residues: 1-124 <EMM>
C:Superfamily: pancreatic ribonuclease
C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F.12/.41.119/Active site: His, Lys, His #status predicted
F./26-.84.40-95.58-110.65-72/Disulfide bonds: #status predicted
F./76/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental

Query Match      21.6%; Score 125; DB 1; Length 124;
Best Local Similarity 28.6%; Pred. No. 1.5e-05;
Matches 34; Conservative 15; Mismatches 42; Indels 28; Gaps 6;

Oy 4 LTFOKHLLTNTRDVD-----CNNIMSTNFL--HCKDKNFYISRPEPVKICKGIISK 55
    |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 6 MKFORQHMDSCNSPGNNPNYCNOHMMRRKRKTGCRKPVNPFVHESLEDAKVC---SQK 61

Oy 56 NVL-----TTSEFYLSDCNVTSRP---CKYKLKKSTNTFCVTENO--APVHF 98
    |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 62 NVLCXNGRTNCYESNSTWHITDRCROTGSKYPRCAVKTSQEKHHIYVACEENPVPVPHF 120

RESULT 10
NRKS
pancreatic ribonuclease (EC 3.1.27.5) - castragwa
C:Species: Proechimys guairae (castragwa)
C>Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 30-Sep-1993
C:Accession: A00821
R:Beintema, J.J.; Knol, G.; Matrena, B.
Biochim. Biophys. Acta 705, 102-110, 1982
A>Title: The primary structures of pancreatic ribonucleases from African porcine and c
A:Reference number: A90644; MUID:83000399; PMID:7115727
A:Accession: A00821
A:Molecule type: protein
A:Residues: 1-128 <BR>
C>Note: residues 67-78 were positioned primarily by homology with other ribonucleases
C:Superfamily: pancreatic ribonuclease
C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F.12/.41.119/Active site: His, Lys, His #status predicted
F./26-.84.40-95.58-110.65-72/Disulfide bonds: #status predicted
F./34/Binding site: carbohydrate (Asn) (covalent) #status experimental

```


Qy	30	CKKNTETIYRPREPAVIAICK---GIASKRV-LTTEEFYISDCNTS---RCCKYKXK	81
Db	39	CKDTNTEFVHNGKSIKDYCEDKDKGKPYKQKFRISKSSFYTTCKAHVGGSPWPCRRIRATS	98
Qy	82	STNTFCVTCENQAPVHF	98
	:	:	:
Db	99	GSRNIVYIACENGGLPVHF	115

RESULT 15

pancreatic ribonuclease (EC 3.1.27.5) - capybara
N:Alternate names: RNase 1; RNase A
C:Species: Hydrochaeris hydrochaeris (capybara, carpincho)
C:Date: 03-Aug-1984 #sequence_revision 03-Aug-1984 #text_change 29-Oct-1999
C:Accession: A00824
R:Reinema, J.J.; Neuteboom, B.
J.Mol. Evol. 19, 145-152, 1983
A:Title: Origin of the duplicated ribonuclease gene in guinea-pig: comparison of the amino acid sequence with that of the guinea-pig and human pancreatic ribonuclease
A:Reference number: A92957; MUID:87036770; PMID:6571219
A:Accession: A00824
A:Molecule type: protein
A:Residues: 1-128 <BEI>
C:Superfamily: pancreatic ribonuclease
C:Keywords: hydrolase; nucleic acid digestion; pancreas
E:12, 41, 119/Active site: His, Lys, His #status predicted
F:26-84, 40-95, 58-110, 65-72/Disulfide bonds: #status predicted

Query Match	Score	DB 1;	Length
20.18;	116;		128;
Best Local Similarity:	37.94;	Prod No. 0 00013	

Best Local Similarity 27.8%; Pred. No. 0.00013;
Matches 32; Conservative 21; Mismatches 42; Indels 20; Gaps 6;

[illegible]

Search completed: January 22, 2004, 12:03:20
Job time : 11.6854 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 22, 2004, 12:01:20 (without alignment)
784.758 Million cell updates/sec

Title: US-09-622-613C-2
Perfect score: 578
Sequence: 1 QDWLTFQKXILTRDVDCN.....TFCVTCENQAPHFVGVGHC 104

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	556	96.2	104	1	RN30_RANPI
2	292	50.5	111	1	RNPQ_RANCA
3	285.5	49.4	111	1	LECS_RANCA
4	269.5	46.6	111	1	RNPPL_RANCA
5	149	25.8	119	1	RNP_IGUG
6	131	22.7	124	1	RNP_GALMU
7	130.5	22.6	145	1	ANGR_MOUSE
8	130.5	22.6	146	1	ANGI_CERAE
9	128	22.1	148	1	ANGI_BOVIN
10	126	21.8	128	1	RNP_MYOCO
11	125	21.6	124	1	RNP_BALAC
12	121.5	21.0	146	1	ANGI_MACMU
13	120	20.7	128	1	RNP_BROCU
14	119.5	20.7	145	1	ANGI_MOUSE
15	119	20.6	128	1	RNPB_CAVPO
16	118.5	20.5	146	1	ANGI_PAPHA
17	117	20.2	124	1	RNP_CHIRR
18	116	20.1	125	1	ANGI_RABIT
19	116	20.1	128	1	RNP_HYDXY
20	114	19.7	124	1	RNP_HIPAM
21	114	19.7	146	1	ANGI_MIOTA
22	113	19.6	147	1	ANGI_HUMAN
23	113	19.6	147	1	ANGI_PANTR
24	112	19.4	150	1	RNP_PIG
25	112	19.4	150	1	RNP_BOVIN
26	112	19.4	156	1	RNP_MYOCU
27	111.5	19.3	147	1	RNS4_HUMAN
28	111	19.2	128	1	RNP_HORSE
29	111	19.2	156	1	RNP_HYSCR
30	111	19.2	156	1	ECPI_MOUSE
31	111	19.2	167	1	RNBR_BOVIN
32	110.5	19.1	123	1	ANGI_PIG
33	110.5	19.1	155	1	ECPI_MOUSE

ALIGNMENTS

34	110	19.0	141	1	RNBR_GIRCA	029542 giraffa cam
35	110	19.0	146	1	ANGI_SACOE	08w62 baguinus oe
36	110	19.0	151	1	RNBR_AXTR	P87350 axis porc
37	109	18.9	123	1	ANG2_BOVIN	P80929 bos tauru
38	109	18.9	124	1	RNPA_CAVPO	P00678 cavia porce
39	109	18.9	124	1	RNP_AEPME	P07847 aepyceros m
40	109	18.9	124	1	RNP_ANTAM	P00668 antilocapra
41	109	18.9	124	1	RNP_SHEEP	P00661 ovis arie
42	109	18.9	146	1	ANGI_SAISC	08w60 saimiri bcl
43	108.5	18.8	156	1	RNS6_SAISC	O46529 saimiri bcl
44	108	18.7	124	1	RNP_BUBBU	P00657 bubalus bub
45	108	18.7	124	1	RNP_CONTA	P00660 connochaete

AC	P22069	STANDARD	PRT	104 AA.
DT	01-AUG-1991 (Rel. 19, Created)			
DT	01-FEB-1994 (Rel. 28, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	P-30 protein (EC 3.1.27.-) (Onconase).			
OS	Rana pipiens (Northern leopard frog).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana;			
OX	NCBI_TaxID=8404;			
RN	[1]			
RP	SEQUENCE.			
RC	TISUB=Embryo;			
RX	MEDLINE=91053131; Pubmed=1985896;			
RA	Ardelt W., Mikulski S.M., Shogen K.;			
RT	"Amino acid sequence of an anti-tumor protein from Rana pipiens			
RT	oocytes and early embryos. Homology to pancreatic ribonucleases.";			
RL	J. Biol. Chem. 266:245-251(1991).			
RN	[2]			
RP	3D-STRUCTURE MODELING.			
RX	MEDLINE=93066156; Pubmed=1438177;			
RA	Mosimann S.C., Johns K.L., Ardelt W., Mikulski S.M., Shogen K.;			
RT	James M.N.G.;			
RT	"Comparative molecular modeling and crystallization of P-30 protein:			
RT	a novel anticancer protein of Rana pipiens oocytes and early			
RL	embryos.";			
RN	Proteins 14:392-400(1992).			
RN	[3]			
RP	X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).			
RX	MEDLINE=94166079; Pubmed=8120892;			
RA	Mosimann S.C., Ardelt W., James M.N.G.;			
RT	"Refined 1.7 A X-ray crystallographic structure of P-30 protein, an			
RT	amphibian ribonuclease with anti-tumor activity.";			
RL	J. Mol. Biol. 236:1141-1153(1994).			
CC	-1- FUNCTION: BASIC PROTEIN WITH ANTIPROLIFERATIVE/CYTOTOXIC ACTIVITY			
CC	AGAINST SEVERAL TUMOR CELL LINES IN VITRO. AS WELL AS ANTITUMOR			
CC	IN VIVO. IT EXHIBITS A RIBONUCLEASE-LIKE ACTIVITY AGAINST HIGH			
CC	MOLECULAR WEIGHT RIBOSOMAL RNA.			
CC	-1- DEVELOPMENTAL STAGE: EARLY EMBRYOS (UP TO FOUR BLASTOMERE STAGE).			
CC	-1- SIMILARITY: Belongs to the pancreatic ribonuclease family.			
DR	Interpro: IPR001427; RNaseA.			
DR	Pfam: PF00074; RNaseA.1.			
DR	ProDom: PD000535; RNaseA.1.			
DR	SMART: SM00092; RNase_PC.1.			
DR	PROSITE: PS00127; RNASE_PANCREATIC.1.			
KW	Hydrolase; Nuclease; Endonuclease; 3D-structure;			
KW	Pyroliidone carboxylic acid.			
FT	MOD_RES	1		
FT	ACT_SITE	10	10	
FT	ACT_SITE	31	31	
FT	ACT_SITE	97	97	
FT	DISULFID	19	68	
FT	DISULFID	30	75	

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FT DISULFID 48 90
FT DISULFID 87 104
FT HELIX 3 10
FT STRAND 11 12
FT HELIX 19 22
FT TURN 23 24
FT TURN 26 30
FT STRAND 33 38
FT HELIX 41 45
FT HELIX 46 48
FT TURN 49 50
FT STRAND 55 58
FT STRAND 63 70
FT TURN 74 75
FT STRAND 77 84
FT STRAND 86 91
FT TURN 92 93
FT STRAND 94 101
SQ SEQUENCE 104 AA; 11845 MW; 22A753C2F9E566B4 CRC64;

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Query Match 96.2%; Score 556; DB 1; Length 104;
Best Local Similarity 96.2%; Pred. No. 1,6e-52;
Matches 100; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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Oy 1 OQMLTFOKHILNTRDVCNNIMSTNLFPHCKDNTFIYSRPEPVKAICKGIISKVLT 60
Db 1 QQMLTFOKHILNTRDVCNNIMSTNLFPHCKDNTFIYSRPEPVKAICKGIISKVLT 60
Oy 61 SEFYLSDCNVTSPCKYKLLKSTNTFCVTCENQAPVHFGVGHIC 104
Db 61 SEFYLSDCNVTSPCKYKLLKSTNTFCVTCENQAPVHFGVGHIC 104

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RESULT 2

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ID RNPO_RANCA STANDARD; PRT; 111 AA.
AC P11916;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ribonuclease, oocytes (EC 3.1.27.-) (RC-RNase) (Sialic acid-binding
DE lectin) (SBL-C).
OS Rana catesbeiana (Bull. frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
OX NCBI_TaxId=8400;
RN [1]
RP SEQUENCE.
RC TISSUE=Egg;
RX MEDLINE=87299649; PubMed=3304421;
RA Titani K., Takio K., Kuwada M., Nitta K., Sakakibara F., Kawauchi H.,
RA Takayanagi G., Hakomori S.;
RA "Amino acid sequence of sialic acid binding lectin from frog (Rana
RT catesbeiana) eggs.";
RL Biochemistry 26:2189-2194(1987).
RN [2]
RN CHARACTERIZATION, AND SEQUENCE OF 59-79.
RX MEDLINE=92220613; PubMed=1373237;
RA Liao Y.-D.;
RA "A pyrimidine-guanine sequence-specific ribonuclease from Rana
RT catesbeiana (bullfrog) oocytes.";
RL Nucleic Acids Res. 20:1371-1377(1992).
RN [3]
RN CHARACTERIZATION.
RC TISSUE=Egg;
RX MEDLINE=93192604; PubMed=8448385;
RA Nitta K., Oyama F., Oyama R., Sekiguchi K., Kawauchi H.,
RA Takayanagi Y., Hakomori S., Titani K.;
RA "Ribonuclease activity of sialic acid-binding lectin from Rana
RT catesbeiana eggs.";
RL Glycobiology 3:37-45(1993).
RN [4]
RN STRUCTURE BY NMR.

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RX MEDLINE=98437383; PubMed=9761686;
RA Chang C.-F., Chen C., Chen Y.-C., Hom K., Huang R.-F., Huang T.H.;
RA "The solution structure of a cytosolic ribonuclease from the oocytes
RT of Rana catesbeiana (bullfrog).";
RL J. Mol. Biol. 283:231-244(1998).
CC -1- FUNCTION: Preferentially cleaves single-stranded RNA at pyrimidine
CC as substrates, and prefers the former. The 5-lectins in frog eggs
CC may be involved in the fertilization and development of the frog
CC embryo. This lectin agglutinates various animal cells, including
CC normal lymphocytes, erythrocytes, and fibroblasts of animal and
CC human origin.
CC -1- SUBUNIT: Monomer.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the pancreatic ribonuclease family.
DR PIR; A27121; A27121.
DR PDB; 1BC4; 28-OCT-98.
DR PDB; 1M07; 21-JAN-03.
DR InterPro; IPR001427; RNASEA.
DR Pfam; PF00074; rnaasea; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_Pc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Hydroxylase; Nuclease; Endonuclease; Sialic acid; Lectin; 3D-structure;
KW Pyroliidone carboxylic acid.
FT MOD RES 1 1
FT ACT_SITE 10 10
FT ACT_SITE 35 35
FT ACT_SITE 103 103
FT DISULFID 19 71
FT DISULFID 34 81
FT DISULFID 52 96
FT DISULFID 93 110
FT HELIX 3 10
FT HELIX 19 23
FT TURN 26 27
FT TURN 37 41
FT STRAND 45 51
FT TURN 52 52
FT STRAND 57 62
FT STRAND 68 73
FT STRAND 83 88
FT STRAND 92 97
FT TURN 98 99
FT STRAND 100 107
SQ SEQUENCE 111 AA; 12464 MW; 0BC9E5F5729ECF4 CRC64;
Query Match 50.5%; Score 292; DB 1; Length 111;
Best Local Similarity 49.5%; Pred. No. 2.1e-24;
Matches 55; Conservative 16; Mismatches 32; Indels 8; Gaps 3;
Oy 1 OQMLTFOKHILNTRDVCNNIMSTNLF---HCKDKNTFIYSRPEPVKAICKGIISKV 56
Db 1 QQMLTFOKHILNTRDVCNNIMSTNLF---HCKDKNTFIYSRPEPVKAICKGIISKV 59
Oy 57 VLTTSEFYLSDC--NVTSPCKYKLLKSTNTFCVTCENQAPVHFGVGHIC 104
Db 60 VLSTFRQALNCTKRISITPRPCYSRTETNIVCVGCENQAPVHFGVGHIC 110

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RESULT 3

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ID LECES_RANJA STANDARD; PRT; 111 AA.
AC P18839;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Sialic acid-binding lectin (EC 3.1.27.-).
OS Rana japonica (Japanese redbellied frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
OX NCBI_TaxId=8402;
RN [1]

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RP SEQUENCE, AND DISULFIDE BONDS.
RC TISSUE=Egg;
RA MEDLINE=91035319; PubMed=2229005;
RA Kamuya Y., Oyama F., Oyama R., Sakakibara F., Nitta K., Kawachi H.,
RA Takayanagi Y., Tlanti K.;
RT "Amino acid sequence of a lectin from Japanese frog (Rana japonica)
eggs."
RL J. Biochem. 108:139-143(1990).
CC -1- FUNCTION: THE S-LECTINS IN FROG EGGS MAY BE INVOLVED IN THE
CC FERTILIZATION AND DEVELOPMENT OF THE FROG EMBRYO. THIS LECTIN
CC PREFERENTIALLY AGGLUTININATE A LARGE VARIETY OF TUMOR CELLS, BUT IT
CC DOES NOT AGGLUTININATE NON-TRANSFORMED CELLS AND ERYTHROCYTES.
CC -1- SUBUNIT: Monomer.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the pancreatic ribonuclease family.
CC PIR: JX0120; JX0120.
DR HSSP: P11916; 1BC4.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; RNaseA; 1.
DR Prodom: PD000535; RNaseA; 1.
DR SMART: SM00092; RNase_Pc; 1.
DR PROSITE: PS00127; RNASE_PANCREATIC; 1.
KW Hydrolyase; Nuclease; Endonuclease; Sialic acid; Lectin;
KW Pyrolydione carboxylic acid.
FT MOD_RES 1 1 PYROLYDIONE CARBOXYLIC ACID.
FT ACT_SITE 10 10 BY SIMILARITY.
FT ACT_SITE 35 35 BY SIMILARITY.
FT ACT_SITE 104 104 BY SIMILARITY.
FT DISULFID 19 72 BY SIMILARITY.
FT DISULFID 34 82
FT DISULFID 52 97
FT DISULFID 94 111
SQ SEQUENCE 111 AA; 12326 MW; FDEBDDF3834ED679 CRC64;

Query Match 49.4%; Score 285.5; DB 1; Length 111;
Best Local Similarity 45.0%; Pred. No. 1e-23;
Matches 50; Conservative 19; Mismatches 35; Indels 7; Gaps 2;

QY 1 QDWLTFQKHLTNTRDVDCNNIMSTNLF---HCKDKNTFTYSRPEPVKAIKGIASKN 56
DB 1 QNMAKFKQKHIRTSISIDNTIMDKAIYIVGCKKERNTFTIISSEDNVKAICSGSPRK 60
QY 57 VLTSEFYLSDC---NTSRPCKYKLLKSTNTFCVTGCNQPVPVGVGHC 104
DB 61 VLTSTRFLNLTGIRSATAPRCPYNSRTETNVIQVCKENRLLPVHFGIGRC 111

RESULT 4
RNP_LIGUG STANDARD; PRT; 111 AA.
ID RNP_LIGUG
AC P14626;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DB Ribonuclease; Liver (EC 3.1.27.5).
DB Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
OC NCBI_TaxID=8400;
RN PIR: S41111; S41111.
RP SEQUENCE.
RC TISSUE=Liver;
RA MEDLINE=90130374; PubMed=2613682;
RA Nitta R., Katayama N., Okabe Y., Iwama M., Watanabe H., Abe Y.,
RA Okazaki T., Ohgi K., Irie M.;
RT "Primary structure of a ribonuclease from bullfrog (Rana catesbeiana)
liver."
RL J. Biochem. 106:729-735(1989).
CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
CC phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
CC with 2',3'-cyclic phosphate intermediates.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the pancreatic ribonuclease family.

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DR PIR: JX0085; JX0085.
DR HSSP: P11916; 1BC4.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; RNaseA; 1.
DR Prodom: PD000535; RNaseA; 1.
DR SMART: SM00092; RNase_Pc; 1.
DR PROSITE: PS00127; RNASE_PANCREATIC; 1.
KW Hydrolyase; Nuclease; Endonuclease; Pyrolydione carboxylic acid.
KW Pyrolydione carboxylic acid.
FT MOD_RES 1 1 PYROLYDIONE CARBOXYLIC ACID.
FT ACT_SITE 10 10 BY SIMILARITY.
FT ACT_SITE 35 35 BY SIMILARITY.
FT ACT_SITE 104 104 BY SIMILARITY.
FT DISULFID 19 72 BY SIMILARITY.
FT DISULFID 34 82 BY SIMILARITY.
FT DISULFID 52 97 BY SIMILARITY.
FT DISULFID 94 111 PROBABLE.
SQ SEQUENCE 111 AA; 12461 MW; D64BA72456C10788 CRC64;

Query Match 46.6%; Score 269.5; DB 1; Length 111;
Best Local Similarity 43.2%; Pred. No. 5.2e-22;
Matches 48; Conservative 19; Mismatches 37; Indels 7; Gaps 2;

QY 1 QDWLTFQKHLTNTRDVDCNNIMSTNLF---HCKDKNTFTYSRPEPVKAIKGIASKN 56
DB 1 QNMAKFKQKHIRTSISIDNTIMDKAIYIVGCKKERNTFTIISSEDNVKAICSGSPRK 60
QY 57 VLTSEFYLSDC---NTSRPCKYKLLKSTNTFCVTGCNQPVPVGVGHC 104
DB 61 ELSTSFYLTNLTGIRSATAPRCPYNSRTETNVIQVCKEKOLPVHFGIGRC 111

RESULT 5
RNP_LIGUG STANDARD; PRT; 119 AA.
ID RNP_LIGUG
AC P80287;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DB Ribonuclease Pancreatic (EC 3.1.27.5) (Rnase 1) (Rnase A).
OC Igwana igwana (Common igwana).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodactylidae; Squamata; Iguania; Iguanidae; Iguaninae; Iguana.
OC NCBI_TaxID=8517;
RN PIR: S41111; S41111.
RP SEQUENCE.
RC TISSUE=Pancreeas;
RA MEDLINE=94139745; PubMed=8307028;
RA Zhao W., Beintema J.J., Hofsteenge J.;
RT "The amino acid sequence of igwana (Iguana igwana) pancreatic
ribonuclease."
RL Eur. J. Biochem. 219:641-646(1994).
CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
CC phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
CC with 2',3'-cyclic phosphate intermediates.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Pancreas.
CC -1- SIMILARITY: Belongs to the pancreatic ribonuclease family.
CC PIR: S41111; S41111.
DR HSSP: P00656; 1LSQ.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; RNaseA; 1.
DR PRINTS: PR00794; RIBONUCLEASE.
DR Prodom: PD000535; RNaseA; 1.
DR SMART: SM00092; RNase_Pc; 1.
DR PROSITE: PS00127; RNASE_PANCREATIC; 1.
KW Hydrolyase; Nuclease; Endonuclease; Pyrolydione carboxylic acid.
KW Pyrolydione carboxylic acid.
FT MOD_RES 1 1 PYROLYDIONE CARBOXYLIC ACID.
FT DISULFID 25 80 BY SIMILARITY.
FT DISULFID 39 91 BY SIMILARITY.
FT DISULFID 57 106 BY SIMILARITY.
FT DISULFID 10 10 BY SIMILARITY.
FT ACT_SITE 40 40 BY SIMILARITY.
FT ACT_SITE 113 113 BY SIMILARITY.

```

SO SEQUENCE 119 AA; 13324 MW; 6072F85B7B15BD5A CRC64;

Query Match 25.8%; Score 149; DB 1; Length 119;
Best Local Similarity 30.7%; Pred. No. 3.7e-09;
Matches 35; Conservative 19; Mismatches 44; Indels 16; Gaps 5;

QY 1 QWLTFRQKHL-----TTRDVDCNNIM---STNLFHCKDKNTFYISRPPEVKAIC--K 49
DB 1 QWMSFQNGHIDYPTETASNPAYCDLMQORNLNPTKCTRTNFVHASPSEIQOVCGSG 60
QY 50 GIASKNVLTTSF-FYLSDC---NVTSPCKYKLLKSTNFCVCENQAPVHF 98
DB 61 GTHYEDNLDSNESFDLTDCKNVGTAPSSCKNGTPIGTRIKRIACENQPVHF 114

RESULT 6

RNP_GALMU STANDARD; PRT; 124 AA.

AC P00680; 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).
GN RNASE1 OR RNS1.
OS Galea musteloides (Cuiis).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriognathi; Cavidae; Galea.
OX NCBI_Taxid=10146;
RN (1) _SEQUENCE.
RX MEDLINE=87036770; PubMed=6571219;
RA Beintema J.J., Neuteboom B.;
RT "Origin of the duplicated ribonuclease gene in guinea-pig: comparison of the amino acid sequences with those of two close relatives: capybara and cuiis ribonuclease.";
RT J. Mol. Evol. 19:145-152(1983).
CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-phosphates and 3'-phosphooligonucleotides ending in C-P or U-P with 2',3'-cyclic phosphate intermediates.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Pancreas.
CC -1- SIMILARITY: Belongs to the pancreatic ribonuclease family.
DR PIR; A00827; NRU1.
DR HSSP; P00656; ISRN.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaaseA.1.
DR PRINTS; PR00794; RIBONUCLEASE.
DR ProDom; PD000535; RIBONUCLEASE.
DR SMART; SM00092; RNase_Pc.1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KM Hydrolyase; Nuclease; Endonuclease.
FT DISULFID 26 84 BY SIMILARITY.
FT DISULFID 40 95 BY SIMILARITY.
FT DISULFID 58 110 BY SIMILARITY.
FT DISULFID 65 72 BY SIMILARITY.
FT ACT_SITE 12 12 BY SIMILARITY.
FT ACT_SITE 41 41 BY SIMILARITY.
FT ACT_SITE 119 119 BY SIMILARITY.
FT VARIANT 1 1 MISSING (IN 1/3 OF THE MOLECULES).
SQ SEQUENCE 124 AA; 13870 MW; 609C7E251A7BA25 CRC64;

Query Match 22.7%; Score 131; DB 1; Length 124;
Best Local Similarity 30.6%; Pred. No. 3.2e-07;
Matches 37; Conservative 18; Mismatches 34; Indels 32; Gaps 7;

QY 4 LTRQKHL-----TTRDVDCNNIM---STNLFHCKDKNTFYISRPPEVKAICKGIIA 53
DB 6 MKFORQHMDSGDHPDNTNIN--YCENEMVRRSMTOGCKPVTVEHPELEAVQAVC-----S 59
QY 54 SKNV-----LTTSEFYLSDCNVTSRP-----CKYKLLKSTNFCVCENQAPVHF 97
DB 60 QKAVPCKNGCTNCTQSHSSMRITDCRYTSSSKYPNCSTYRMTQAKSIIYACGTPSVPVH 119

QY 98 F 98
DB 120 F 120

RESULT 7

ANGR_MOUSE STANDARD; PRT; 145 AA.

AC 064438; 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Angiogenin-related protein precursor.
GN ANGRP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN (1) _SEQUENCE FROM N.A.
RX STRAIN=129; TISSUE=Liver;
RX MEDLINE=96079109; PubMed=8530072;
RA Brown W.E., Noble V., Subramanian V., Shapiro R.;
RT "The mouse angiogenin gene family: structures of an angiogenin-related protein gene and two pseudogenes";
RT Genomics 29:200-206(1995).
CC -1- SIMILARITY: Belongs to the pancreatic ribonuclease family.
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CC DR EMBL; U22519; AAA91367.1; -
DR HSSP; P03950; 1A4Y.
DR MOD; MG1:104984; AngRP.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaaseA.1.
DR PRINTS; PR00794; RIBONUCLEASE.
DR ProDom; PD000535; RIBONUCLEASE.
DR SMART; SM00092; RNase_Pc.1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KM Signal; Hydrolyase; Nuclease; Endonuclease;
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 145 ANGIOGENIN-RELATED PROTEIN.
FT MOD_RES 25 25 PYROLIDONE CARBOXYLIC ACID (BY SIMILARITY).
FT ACT_SITE 37 37 BY SIMILARITY.
FT ACT_SITE 64 64 BY SIMILARITY.
FT ACT_SITE 137 137 BY SIMILARITY.
FT DISULFID 50 104 BY SIMILARITY.
FT DISULFID 63 115 BY SIMILARITY.
FT DISULFID 81 130 BY SIMILARITY.
SQ SEQUENCE 145 AA; 16612 MW; 29A6EB814429C4AD CRC64;

Query Match 22.6%; Score 130.5; DB 1; Length 145;
Best Local Similarity 38.2%; Pred. No. 4.3e-07;
Matches 29; Conservative 11; Mismatches 29; Indels 7; Gaps 3;

QY 30 CQDKNTFYISRPPEVKAIC--KGIASKNV-LTTSEFYLSDCNVTSR-----PCKYLLKKS 82
DB 63 CQDVNTFHIDTQNNIYAIKGGKSPYGRMLRISKSRFYQVTTCTHKGSRPRPCRYASKG 122
QY 83 TMTFCVTCENQAPVHF 98
DB 123 FRTIITGCGNVPVHF 138

RESULT 8

NGI_CEREA	STANDARD:	PRT:	146 AA.
AC	08MAR6;		
DT	28-FEB-2003 (Rel. 41, Created)		
DT	28-FEB-2003 (Rel. 41, Last sequence update)		
DT	28-FEB-2003 (Rel. 41, Last annotation update)		
DE	Angiogenin precursor (EC 3.1.27.-) (Ribonuclease 5) (RNase 5).		
GN	ANG OR RNASE5.		
OS	Cercopithecus aethiops (Green monkey) (Grivet).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;		
OC	Cercopithecinae; Cercopithecus.		
OX	NCBI_TaxID=9534;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=21918422; PubMed=11919285;		
RA	Zhang J., Rosenberg H.F.;		
RT	"Divergelying selection of the tumor-growth promoter angiogenin in		
RT	primate evolution.";		
RL	Mol. Biol. Evol. 19:438-445(2002).		
CC	-I- FUNCTION: MAY FUNCTION AS A TRNA-SPECIFIC RIBONUCLEASE THAT BINDS		
CC	TO ACTIN ON THE SURFACE OF ENDOTHELIAL CELLS; ONCE BOUND,		
CC	ANGIOGENIN IS ENDOCYTOSED AND TRANSLOCATED TO THE NUCLEUS, THEREBY		
CC	PROMOTING THE ENDOTHELIAL INVASIVENESS NECESSARY FOR BLOOD VESSEL		
CC	FORMATION. ANGIOGENIN INDUCES VASCULARIZATION OF NORMAL AND		
CC	MALIGNANT TISSUES. ABOLISHES PROTEIN SYNTHESIS BY SPECIFICALLY		
CC	HYDROLYZING CELLULAR TRNAs (By similarity).		
CC	-I- SUBCELLULAR LOCATION: Secreted.		
CC	-I- SIMILARITY: Belongs to the pancreatic ribonuclease family.		
CC	-----		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration		
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -		
CC	the European Bioinformatics Institute. There are no restrictions on its		
CC	use by non-profit institutions as long as its content is in no way		
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CC	entities requires a license agreement (See http://www.isb-sdb.ch/announce/		
CC	or send an email to license@isb-sdb.ch).		
CC	-----		
DR	EMBL; AF441664; AAL1646.1; -		
DR	InterPro; IPR001427; RNaseA.		
DR	Pfam; PF00074; rnaaseA; 1.		
DR	ProDom; PD000535; RNaseA; 1.		
DR	SMART; SM00092; RNase_Pc; 1.		
DR	PROSITE; PS00127; RNASE_PANCREATIC; 1.		
KM	Hydrolase; Nuclease; Endonuclease; Angiogenesis;		
KW	Protein synthesis inhibitor; Signal; Pyroglutamate carboxylic acid.		
FT	SIGNAL	1	24
FT	CHAIN	25	146
FT	MOD_RES	25	25
FT			
FT	ACT_SITE	37	37
FT	ACT_SITE	64	64
FT	ACT_SITE	138	138
FT	DISULFID	50	105
FT	DISULFID	63	116
FT	DISULFID	81	131
SO	SEQUENCE	146 AA;	16444 MW; 27860112858BDP9 CRC64;
Query Match	22.6%;	Score 130.5;	DB 1; Length 146;
Best Local Similarity	30.7%;	Pred. No. 4.4e-07;	
Matches	31;	Conservative 17;	Mismatches 30; Indels 23; Gaps 4;
OY	5	TFQKKHLLTRDVQCNINMSTNLHCHDKKNTFYSRREPVAIC---KGITASKV-LTT 60	
DB	53	TMRRRLHLLSP-----CXDINFFHGNNRHIIKAIIGDENGNGPYGENTLRISK 97	
OY	61	SEFYLSDCNVTST---RPCKYKLKSTVTPCVTGENQAPVH 97	
DB	98	SPFOVTTCNLRGSGPRPCYCARATRGSGNIVVGENGLPVH 138	

ID	ANGI BOVIN	STANDARD:	PRT:	148 AA.
AC	P10152; Q9GK99;			
AD	01-MAR-1969 (Rel. 10, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Angiogenin-1 precursor (EC 3.1.27.-).			
GN	ANGI OR ANG.			
OS	Bos taurus (bovine).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;			
OC	Bovidae; Bovinae; Bos.			
OX	NCBI_TaxID=9913;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Liver;			
RA	Chang S.-I.;			
RT	"Cloning, sequencing, and expression of bovine angiogenin.";			
RL	Submitted (MAR-1999) to the EMBL/Genbank/DBJ databases.			
RN	[2]			
RP	SEQUENCE OF 24-148.			
RC	TISSUE=Milk;			
RX	MEDLINE=89065101; PubMed=3197938;			
RA	Maes P., Damerit D., Rommens C., Monteunil J., Spik G., Tartat A.;			
RT	"The complete amino acid sequence of bovine milk angiogenin.";			
RL	FEBS Lett. 241:41-45(1988).			
RN	[3]			
RP	SEQUENCE OF 24-148.			
RC	TISSUE=Plasma;			
RX	MEDLINE=89375344; PubMed=2775757;			
RA	Bond M.D., Strydom D.J.;			
RT	"Amino acid sequence of bovine angiogenin.";			
RL	Biochemistry 28:6110-6113(1989).			
RN	[4]			
RP	CHARACTERIZATION, AND SEQUENCE OF 25-55.			
RC	TISSUE=Plasma;			
RX	MEDLINE=89118214; PubMed=3064806;			
RA	Bond M.D., Vallee B.L.;			
RT	"Isolation of bovine angiogenin using a placental ribonuclease			
RL	inhibitor binding assay.";			
RN	Biochemistry 27:6282-6287(1988).			
RN	[5]			
RP	X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS).			
RX	MEDLINE=95224057; PubMed=7708754;			
RA	Acharya K.R., Shapiro R., Riodan J.F., Vallee B.L.;			
RT	"Crystal structure of bovine angiogenin at 1.5-A resolution.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 92:2949-2953(1995).			
RP	[6]			
RC	STRUCTURE BY NMR.			
RA	MEDLINE=96280645; PubMed=8688423;			
RA	Leguin O., Albaret C., Bontems F., Spik G., Lallemand J.-Y.;			
RT	"Solution structure of bovine angiogenin by 1H nuclear magnetic			
RL	resonance spectroscopy.";			
RN	Biochemistry 35:8870-8880(1996).			
CC	-1- FUNCTION: MAY FUNCTION AS A tRNA-SPECIFIC RIBONUCLEASE THAT BINDS			
CC	TO ACTIN ON THE SURFACE OF ENDOTHELIAL CELLS; ONCE BOUND,			
CC	ANGIOGENIN IS ENDOCYTOSED AND TRANSLOCATED TO THE NUCLEUS, THEREBY			
CC	PROMOTING THE ENDOTHELIAL INVASIVENESS NECESSARY FOR BLOOD VESSEL			
CC	FORMATION. ANGIOGENIN INDUCES VASCULARIZATION OF NORMAL AND			
CC	MALIGNANT TISSUES. ABOLISHES PROTEIN SYNTHESIS BY SPECIFICALLY			
CC	HYDROLYZING CELLULAR TRANS. BINDS TIGHTLY TO PLACENTAL			
CC	RIBONUCLEASE INHIBITOR AND HAS VERY LOW RIBONUCLEASE ACTIVITY.			
CC	-1- SUBCELLULAR LOCATION: Secreted.			
CC	-1- TISSUE SPECIFICITY: SERUM, AND MILK.			
CC	-1- SIMILARITY: Belongs to the pancreatic ribonuclease family.			
CC	-----			
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Db 6 MKFORHNDGNSPGNNPNYCNQMMRRKMTGRCCKPVNTFVHESLEBVKAVC-----SQK 61
Oy 56 NVL-----TSEFYLSDCNVTSRP-----CKYKXKKSNTFCVTCENQ--APVHF 98
Db 62 NVLCXNGRTNCTYESNTWHTIDCROTGSCKYPCNCAKTSQEKHIIIVACEGNPVYVHF 120

RESULT 12
ANGI_MACMU STANDARD; PRT; 146 AA.
ID ANGI_MACMU
AC Q8MNE3; 2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE Angiogenin precursor (EC 3.1.27.-) (Ribonuclease 5) (Rnaase 5).
GN ANG OR RNASES.
OS Macaca mulatta (Rheus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21918422; PubMed=1191285;
RA Zhang J., Rosenberg H.F.;
RT "Diversifying selection of the tumor-growth promoter angiogenin in
RL primate evolution."
RT Mol. Biol. Evol. 19:438-445 (2002).
CC -1- FUNCTION: MAY FUNCTION AS A TRNA-SPECIFIC RIBONUCLEASE THAT BINDS
CC TO ACTIN ON THE SURFACE OF ENDOTHELIAL CELLS; ONCE BOUND,
CC ANGIOENIN IS ENDOCYTOSED AND TRANSLOCATED TO THE NUCLEUS, THEREBY
CC PROMOTING THE ENDOTHELIAL INVASIVENESS NECESSARY FOR BLOOD VESSEL
CC FORMATION. ANGIOENIN INDUCES VASCULARIZATION OF NORMAL AND
CC MALIGNANT TISSUES. ABOLISHES PROTEIN SYNTHESIS BY SPECIFICALLY
CC HYDROLYZING CELLULAR TRNAs (by similarity).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the pancreatic ribonuclease family.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: AF41667; AAL61649.1;
DR InterPro: IPR001427; Rnaase.
DR Pfam: PF00074; Rnaase.
DR ProDom: PD000535; Rnaase; 1.
DR SMART: SM00092; Rnaase; 1.
DR PROSITE: PS00127; Rnaase; 1.
KW Hydrolyase; Nuclease; Endonuclease; Angiogenesis;
KM Protein synthesis inhibitor; Signal; Pyrolydione carboxylic acid.
FT SIGNAL 1 24
FT CHAIN 25 146
FT MOD_RSS 25 25
FT ACT_SITE 37 37
FT ACT_SITE 64 64
FT ACT_SITE 138 138
FT DISULFID 50 105
FT DISULFID 63 116
FT DISULFID 81 131
SQ SEQUENCE 146 AA; 16301 MW; E39A89215DB2A2A4 CRC64;

Query Match 21.0%; Score 121.5; DB 1; Length 146;
Best Local Similarity 28.7%; Pred. No. 4e-06;
Matches 29; Conservative 17; Mismatches 32; Indels 23; Gaps 4;

Oy 5 TPOKHLTNTRDVDCNNIMSTNLFHCKDKNTFYISREPKATC--KGIASGNV-LTT 60
Db 53 TMRKRHLTSP-----CKDINTFVGNRHHTAITACGDEGSPYGGNLRIST 97

Oy 61 SEFYLSDCNVT-----RCKYKXKKSNTFCVTCENQAPVH 97
Db 98 SPFOVTTCKLRGSGPRPCQYRATGRSNIVVGCENGLPVH 138

RESULT 13
RNP_PROGU STANDARD; PRT; 128 AA.
ID RNP_PROGU
AC P04059;
DT 01-NOV-1986 (Rel. 03, Created)
DT 01-NOV-1986 (Rel. 03, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ribonuclease pancreatic (EC 3.1.27.5) (Rnaase 1) (Rnaase A).
GN RNASE1 OR RN1.
OS Proechimys guairae (Castiagua).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Echimyidae; Proechimyus.
OX NCBI_TaxID=10163;
RN [1]
RP SEQUENCE.
RC TISSUE=Pancreas;
RX MEDLINE=83000399; PubMed=7115727;
RA Beintema J.J., Knol G., Martena B.;
RT "The primary structures of pancreatic ribonucleases from African
RT porcupine and castiagua, two hystricomorph rodent species."
RL Biochim. Biophys. Acta 703:102-110 (1982).
CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
CC phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
CC with 2',3'-cyclic phosphate intermediates.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Pancreas.
CC -1- SIMILARITY: Belongs to the pancreatic ribonuclease family.
CC PIR: A00821; NRNS.
DR HSSP: P00656; ISRN.
DR InterPro: IPR001427; Rnaase.
DR Pfam: PF00074; Rnaase; 1.
DR PRINTS: PR00794; RIBONUCLEASE.
DR ProDom: PD000535; Rnaase; 1.
DR SMART: SM00092; Rnaase; 1.
DR PROSITE: PS00127; Rnaase; 1.
KW Hydrolyase; Nuclease; Endonuclease; Glycoprotein.
FT DISULFID 26 84
FT DISULFID 40 95
FT DISULFID 58 110
FT DISULFID 65 72
FT ACT_SITE 12 12
FT ACT_SITE 41 41
FT ACT_SITE 119 119
FT CARBOHYD 34 34
SQ SEQUENCE 128 AA; 14244 MW; 2DB58093A9D0C936 CRC64;

Query Match 20.8%; Score 120; DB 1; Length 128;
Best Local Similarity 29.9%; Pred. No. 4.9e-06;
Matches 35; Conservative 19; Mismatches 36; Indels 28; Gaps 7;

Oy 6 FOKHLL-----TNTRDVDCNNIM-STNLF--HCKDKNTFYISREPKATCKGIASGNV 57
Db 8 FOROHIDSGSPSTNPYCNAMKMSRMTOERCKPVTFFVHEPLADYQAVC-----FOKNN 63

Oy 58 -----LTTSEFYLSDCNVTSRP-----CKYKXKKSNTFCVTCENQ--APVHF 98
Db 64 PCKXNGSNCYESTSNMHTIDCRLTNSKSPDCLYRISOEKSIIVACEGNPVYVHF 120

RESULT 14
ANGI_MOUSE STANDARD; PRT; 145 AA.
ID ANGI_MOUSE
AC P21570;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Angiogenin precursor (EC 3.1.27.-) (Ribonuclease 5) (Rnaase 5).

```

OS Mus musculus (Mouse) .
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=91025023; PubMed=222458;
RX Bond M.D., Vallée B.L.;
RT "Isolation and sequencing of mouse angiogenin DNA.";
RL Biochem. Biophys. Res. Commun. 171:988-995(1990) .
RN [2]
RP PARTIAL SEQUENCE.
RC TISSUE=Serum;
RX MEDLINE=91192291; PubMed=8448182;
RT Bond M.D., Strydom D.J., Vallée B.L.;
RT "Characterization and sequencing of rabbit, pig and mouse
RT angiogenins: discernment of functionally important residues and
RT regions";
RL Biochim. Biophys. Acta 1162:177-186(1993) .
CC -1- FUNCTION: MAY FUNCTION AS A TRNA-SPECIFIC RIBONUCLEASE THAT BINDS
CC TO ACTIN ON THE SURFACE OF ENDOTHELIAL CELLS; ONCE BOUND,
CC ANGIOENIN IS ENDOCYTOSED AND TRANSLOCATED TO THE NUCLEUS, THEREBY
CC PROMOTING THE ENDOTHELIAL INVASIVENESS NECESSARY FOR BLOOD VESSEL
CC FORMATION. ANGIOENIN INDUCES VASCULARIZATION OF NORMAL AND
CC MALIGNANT TISSUES. ABOLISHES PROTEIN SYNTHESIS BY SPECIFICALLY
CC HYDROLYZING CELLULAR TRNAs.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the pancreatic ribonuclease family.
CC -----
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CC -----
DR EMBL; U22516; AAA91366.1; .
DR PIR; A35932; A35932.
DR HSSP; P03950; 1AAV.
DR MGD; MGI:88022; Ang.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaseA; 1.
DR PRINTS; PR00794; RIBONUCLEASE.
DR PRODOM; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_Pc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Hydroxylase; Nuclease; Endonuclease; Angiogenesis;
KW protein synthesis inhibitor; signal; Pyroglutamate carboxylic acid.
FT SIGNAL 1 24
FT CHAIN 25 145
FT MOD_RES 25 25
FT PT ACT_SITE 37 37
FT ACT_SITE 64 64
FT ACT_SITE 137 137
FT DISULFID 50 104
FT DISULFID 63 115
FT DISULFID 81 130
FT SEQUENCE 145 AA; 16228 MW; 06944260BB764938 CRC64;
SO
Query Match 20.7%; Score 119.5; DB 1; Length 145;
Best Local Similarity 30.8%; Pred. No. 6.4e-06;
Matches 33; Conservative 12; Mismatches 45; Indels 17; Gaps 5.
OY 9 KHLNTRDVD-----CNNIMTNLF--HCKDNTFTYSPREPVAIC--KGIISKN 56
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 32 KFLTQHNDAKPGKDDRYCERMMKRSRLTSPCKDVNTFTLHGKSIKAIKANGSPRYEN 91
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 57 V-LITSEFYLSQCVNTS----RPCKYKLKLSNTNTCVTCENQAPVHF 98
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 92 LRMSASPFOVTTCKRTGGSPRPCCQYRNASAGRRHVAVIVCENGLPVHF 138
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | |

```

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RESULT 15
RNPB_CAVPO STANDARD; PRT; 128 AA.
ID_RNPB_CAVPO          STANDARD;          PRT;    128 AA.
AC      P00679;
DT      21-JUL-1986 (Rel. 01, Created)
DT      21-JUL-1986 (Rel. 01, Last sequence update)
DT      28-FEB-2003 (Rel. 01, Last annotation update)
DE      Ribonuclease pancreatic B (EC 3.1.27.5) (RNase IB).
OS      Cavia porcellus (Guinea pig).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Hystricognathi; Cavidae; Cavia.
OX      NCBI_TaxId=10141;
RN      [1]
RP      SEQUENCE.
RC      TISSUE=Pancreas;
RX      MEDLINE=77185023; PubMed=862624;
RX      van den Berg A., van den Hende-Timmer L., Hofsteenge J., Gaastera W.,
RA      Beintema J.J.;
RL      "Guinea-pig pancreatic ribonucleases. Isolation, properties, primary
RT      structure and glycosidation";
RL      Eur. J. Biochem. 75:91-100(1977).
CC      -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
CC      phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
CC      with 2',3'-cyclic phosphate intermediates.
CC      -1- SUBCELLULAR LOCATION: Secreted.
CC      -1- TISSUE SPECIFICITY: Pancreas.
CC      -1- SIMILARITY: Belongs to the pancreatic ribonuclease family.
DR      PIR: A00826; NRGPB.
DR      HSSP: P00656; ISRN.
DR      InterPro: IPR001427; RNaseA.
DR      Pfam: PF00074; RNaseA. 1.
DR      PRINTS: PR00794; RIBONUCLEASE.
DR      ProDom: PD000535; RNaseA; 1.
DR      SMART: SM00092; RNase_PC; 1.
DR      PROSITE: PS00127; RNASE_PANCREATIC; 1.
KM      Hydroxylase; Nuclease; Endonuclease; Glycoprotein.
FT      DISULFID        26           84       BY SIMILARITY
FT      FT              40           95
FT      DISULFID        58          110       BY SIMILARITY
FT      FT              65          112       BY SIMILARITY
FT      ACT_SITE        12           12
FT      ACT_SITE        41           41       BY SIMILARITY
FT      ACT_SITE        119          119       BY SIMILARITY
FT      CARBOHYD        21            21       N-LINKED (GLCNAC. . .)
FT      CARBOHYD        34            34       L-LINKED (GLCNAC. . .)
FT      VARIANT         64            64       L->P.
SQ      SEQUENCE      128 AA; 14406 MW; AZF4I0IA1AJ3E93B CRC64;

Query Match                20.6%; Score 119; DR 1; Length 128;
Beet Local Similarity      28.3%; Pred. No. 6.3e-06;
Matches   34; Conservative 21; Mismatches 35; Indels 30; Gaps 7;

QY      4 LTFOKPHL-----TNRDVDCNNIM--STNLFHCKDKNTFIYSRDPVKAICKGIIAS 54
      :|::||: |::| |::| |::| |::| |::|
DB      6 MKFGQRQHMDPGSGSNSGNV-CNVMMIRRNITGRCKRPVUTFYHESLADYGAVC----FQ 60
      ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY      55 KVVLT-----TISEFYISDCNVTSRP---CKYLKLKSKTNTPFCVCTENQ--APVHF 98
      ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB      61 KNVLCKNGQTNCYOYSRMRIITDCRVTSISKFPNCYSRMSQAOKSIIVACEGDPYVHVHF 120
      ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

Search completed: January 22, 2004, 12:02:08
Job time : 7.23221 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 22, 2004, 12:02:15 ; Search time 24.7241 Seconds
(without alignments)
869.271 Million cell updates/sec

Title: US-09-622-613C-2
Perfect score: 578
Sequence: 1 QDWLTFOKXHLTNRDVDCN.....TFCVTCENQAPVHFGVGHG 104

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 777136 seqs, 20673638 residues

Total number of hits satisfying chosen parameters: 777136

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubppaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubppaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubppaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubppaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubppaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubppaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubppaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubppaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubppaa/US09_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubppaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubppaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubppaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubppaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubppaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubppaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubppaa/US10C_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/1/pubppaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubppaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	578	100.0	104	11	US-09-961-400-2
2	578	100.0	105	11	US-09-948-391A-6
3	578	100.0	105	11	US-09-961-400-6
4	578	100.0	127	11	US-09-948-391A-28
5	578	100.0	127	11	US-09-961-400-28
6	575	99.5	111	11	US-09-961-400-9
7	573	99.1	104	11	US-09-948-391A-11
8	573	99.1	104	11	US-09-961-400-11
9	573	99.1	105	11	US-09-948-391A-13
10	573	99.1	105	11	US-09-961-400-13
11	569	98.4	104	11	US-09-948-391A-2
12	569	98.4	104	11	US-09-948-391A-4
13	569	98.4	104	11	US-09-961-400-4
14	565	97.8	105	11	US-09-961-400-8
15	560	96.9	105	11	US-09-948-391A-8

16	560	96.9	111	11	US-09-948-391A-9	Sequence 9, Appl1
17	556	96.2	105	15	US-10-153-882-2	Sequence 2, Appl1
18	551	95.3	104	10	US-09-986-119-1	Sequence 1, Appl1
19	551	95.3	104	11	US-09-918-887-1	Sequence 3, Appl1
20	445	77.0	83	10	US-09-986-119-3	Sequence 15, Appl1
21	445	77.0	83	11	US-09-918-887-3	Sequence 15, Appl1
22	281.5	48.7	110	11	US-09-948-391A-15	Sequence 15, Appl1
23	281.5	48.7	110	11	US-09-961-400-15	Sequence 15, Appl1
24	281.5	48.7	110	11	US-09-961-400-17	Sequence 15, Appl1
25	277.5	48.0	110	11	US-09-961-400-19	Sequence 19, Appl1
26	277.5	48.0	111	11	US-09-948-391A-21	Sequence 21, Appl1
27	277.5	48.0	111	11	US-09-961-400-21	Sequence 21, Appl1
28	277.5	48.0	117	11	US-09-948-391A-22	Sequence 22, Appl1
29	277.5	48.0	117	11	US-09-961-400-22	Sequence 22, Appl1
30	276.5	47.8	110	11	US-09-948-391A-24	Sequence 24, Appl1
31	276.5	47.8	110	11	US-09-961-400-24	Sequence 24, Appl1
32	276.5	47.8	111	11	US-09-948-391A-26	Sequence 26, Appl1
33	276.5	47.8	111	11	US-09-961-400-26	Sequence 26, Appl1
34	275.5	47.7	111	11	US-09-948-391A-17	Sequence 17, Appl1
35	271.5	47.0	110	11	US-09-948-391A-19	Sequence 19, Appl1
36	157.5	27.2	169	13	US-10-016-447-2	Sequence 2, Appl1
37	149	25.8	119	12	US-10-074-978A-139	Sequence 139, App
38	128.5	22.2	124	13	US-10-016-447-5	Sequence 5, Appl1
39	113	19.6	147	9	US-09-286-240-6	Sequence 6, Appl1
40	113	19.6	147	9	US-09-863-777-2	Sequence 2, Appl1
41	113	19.6	147	10	US-09-731-872-254	Sequence 254, App
42	113	19.6	147	12	US-09-876-597-254	Sequence 254, App
43	112	18.4	124	10	US-09-981-286A-8	Sequence 8, Appl1
44	106.5	18.4	99	12	US-10-074-978A-141	Sequence 141, App
45	104.5	18.1	89	12	US-10-074-978A-143	Sequence 143, App

ALIGNMENTS

RESULT 1
US-09-961-400-2
Sequence 2, Application US/09961400
Publication No. US20030124131A1
GENERAL INFORMATION:
APPLICANT: RYBAK, SUSANNA M.
APPLICANT: GOLDENBERG, DAVID M.
APPLICANT: NEWTON, DIANNE L.
TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
FILE REFERENCE: 018733/1059
CURRENT APPLICATION NUMBER: US/09/961,400
PRIOR FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: 09/622,613
PRIOR FILING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: PCT/US99/06641
PRIOR FILING DATE: 1998-03-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 104
TYPE: PRT
ORGANISM: Rana pipiens
US-09-961-400-2

Query Match 100.0%; Score 578; DB 11; Length 104;

Best Local Similarity 100.0%; Pred. No. 9, 8e-59;

Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QDWLTFOKXHLTNRDVDCNIMSTNLFHCKDKNTFYSPRPVKAICKGIIASKNVLT 60
DB 1 QDWLTFOKXHLTNRDVDCNIMSTNLFHCKDKNTFYSPRPVKAICKGIIASKNVLT 60
QY 61 SEFYLSDCNVTSPRCYKYLKKSSTNTFCVTCENQAPVHFGVGHG 104
DB 61 SEFYLSDCNVTSPRCYKYLKKSSTNTFCVTCENQAPVHFGVGHG 104

RESULT 2

US-09-948-391A-6
; Sequence 6, Application US/09948391A
; Publication No. US20030027311A1
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: The United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Recombinant Anti-Tumor RNase
; FILE REFERENCE: 015280-343110US
; CURRENT APPLICATION NUMBER: US/09/948,391A
; CURRENT FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 60/079,751
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/622,613
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Rana pipiens
; OTHER INFORMATION: ribonuclease with Met at position 1 (recombinant
US-09-948-391A-6

Query Match 100.0%; Score 578; DB 11; Length 105;
Best Local Similarity 100.0%; Pred. No. 9.9e-59;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ODMLTFOKGLTNTDVCNNIMSTNLFHCKDKNTFTYSRPEPVKAIKGIISKVLT 60
DB 2 ODMLTFOKGLTNTDVCNNIMSTNLFHCKDKNTFTYSRPEPVKAIKGIISKVLT 61
QY 61 SEFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFGVGH 104
DB 62 SEFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFGVGH 105

RESULT 3

US-09-961-400-6
; Sequence 6, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: GOLDENBERG, DAVID M.
; APPLICANT: NEWTON, DIANNE L.
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 018733/1059
; CURRENT APPLICATION NUMBER: US/09/961,400
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 09/622,613
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/079,751
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Rana pipiens
US-09-961-400-6

Query Match 100.0%; Score 578; DB 11; Length 105;
Best Local Similarity 100.0%; Pred. No. 9.9e-59;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ODMLTFOKGLTNTDVCNNIMSTNLFHCKDKNTFTYSRPEPVKAIKGIISKVLT 60
DB 2 ODMLTFOKGLTNTDVCNNIMSTNLFHCKDKNTFTYSRPEPVKAIKGIISKVLT 61
QY 61 SEFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFGVGH 104
DB 62 SEFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFGVGH 105

RESULT 4

US-09-948-391A-28
; Sequence 28, Application US/09948391A
; Publication No. US20030027311A1
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: The United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Recombinant Anti-Tumor RNase
; FILE REFERENCE: 015280-343110US
; CURRENT APPLICATION NUMBER: US/09/948,391A
; CURRENT FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 60/079,751
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/622,613
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
; LENGTH: 127
; TYPE: PRT
; ORGANISM: Rana pipiens
; FEATURE:
; OTHER INFORMATION: Rana pipiens ribonuclease (RapLr1) Clone 5a1b cDNA
; OTHER INFORMATION: insert
US-09-948-391A-28

Query Match 100.0%; Score 578; DB 11; Length 127;
Best Local Similarity 100.0%; Pred. No. 1.2e-58;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ODMLTFOKGLTNTDVCNNIMSTNLFHCKDKNTFTYSRPEPVKAIKGIISKVLT 60
DB 24 ODMLTFOKGLTNTDVCNNIMSTNLFHCKDKNTFTYSRPEPVKAIKGIISKVLT 83
QY 61 SEFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFGVGH 104
DB 84 SEFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFGVGH 127

RESULT 5

US-09-961-400-28
; Sequence 28, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: GOLDENBERG, DAVID M.
; APPLICANT: NEWTON, DIANNE L.
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 018733/1059
; CURRENT APPLICATION NUMBER: US/09/961,400
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 09/622,613
; PRIOR FILING DATE: 2000-08-17

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; PRIOR APPLICATION NUMBER: PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/079,751
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 127
; TYPE: PRT
; ORGANISM: Rana pipiens
US-09-961-400-28
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Query Match          100.0%; Score 578; DB 11; Length 127;
Best Local Similarity 100.0%; Pred. No. 1.2e-58;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 ODMLTFOKKHLTNRDVCNNIMSTNLFHCKDKNTFTYSRPPVKAICKGIIASKNVLT 60
Db 24 ODMLTFOKKHLTNRDVCNNIMSTNLFHCKDKNTFTYSRPPVKAICKGIIASKNVLT 83

Qy 61 SEFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVC 104
Db 84 SEFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVC 127
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RESULT 6
US-09-961-400-9
; Sequence 9, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: GOLDENBERG, DAVID M.
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
; FILE REFERENCE: 018733/1059
; CURRENT APPLICATION NUMBER: US/09/961,400
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 09/622,613
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/079,751
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Rana pipiens
US-09-961-400-9
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Query Match          99.5%; Score 575; DB 11; Length 111;
Best Local Similarity 99.0%; Pred. No. 2.3e-58;
Matches 103; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 ODMLTFOKKHLTNRDVCNNIMSTNLFHCKDKNTFTYSRPPVKAICKGIIASKNVLT 60
Db 8 ODMLTFOKKHLTNRDVCNNIMSTNLFHCKDKNTFTYSRPPVKAICKGIIASKNVLT 67

Qy 61 SEFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVC 104
Db 68 SEFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVC 111
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RESULT 7
US-09-948-391A-11
; Sequence 11, Application US/09948391A
; Publication No. US20030027311A1
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: The United States of America
```

```

; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Recombinant Anti-Tumor RNase
; FILE REFERENCE: 015280-343110US
; CURRENT APPLICATION NUMBER: US/09/948,391A
; CURRENT FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 60/079,751
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/622,613
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 104
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Rana pipiens
; OTHER INFORMATION: ribonuclease with Q18Ser substitution
; OTHER INFORMATION: (recombinant RalRL1 Q18)
US-09-948-391A-11
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Query Match          99.1%; Score 573; DB 11; Length 104;
Best Local Similarity 100.0%; Pred. No. 3.7e-58;
Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 2 DMLTFOKKHLTNRDVCNNIMSTNLFHCKDKNTFTYSRPPVKAICKGIIASKNVLT 61
Db 2 DMLTFOKKHLTNRDVCNNIMSTNLFHCKDKNTFTYSRPPVKAICKGIIASKNVLT 61

Qy 62 EFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVC 104
Db 62 EFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVC 104
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RESULT 8
US-09-961-400-11
; Sequence 11, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: GOLDENBERG, DAVID M.
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
; FILE REFERENCE: 018733/1059
; CURRENT APPLICATION NUMBER: US/09/961,400
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 09/622,613
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/079,751
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 104
; TYPE: PRT
; ORGANISM: Rana pipiens
US-09-961-400-11
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```

Query Match          99.1%; Score 573; DB 11; Length 104;
Best Local Similarity 100.0%; Pred. No. 3.7e-58;
Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 2 DMLTFOKKHLTNRDVCNNIMSTNLFHCKDKNTFTYSRPPVKAICKGIIASKNVLT 61
Db 2 DMLTFOKKHLTNRDVCNNIMSTNLFHCKDKNTFTYSRPPVKAICKGIIASKNVLT 61

Qy 62 EFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVC 104
```

Db 62 EFYLSDCNVTSRPCKYKLLKKSNTNFCVTCENQAPVHFVGHC 104

RESULT 9
US-09-948-391A-13

Sequence 13, Application US/09948391A
Publication No. US20030027311A1
GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: The United States of America
APPLICANT: as represented by The Secretary of the
Department of Health and Human Services
TITLE OF INVENTION: Recombinant Anti-Tumor RNase
FILE REFERENCE: 015280-343110US
CURRENT APPLICATION NUMBER: US/09/948,391A
CURRENT FILING DATE: 2002-05-10
PRIOR APPLICATION NUMBER: US 60/079,751
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: WO PCT/US99/06641
PRIOR FILING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: US 09/622,613
PRIOR FILING DATE: 2000-08-17
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 13
LENGTH: 105
TYPE: PRF
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Rana pipiens
OTHER INFORMATION: ribonuclease with Met at position 1 and Glu25er
OTHER INFORMATION: substitution (recombinant Met(-1) RapiR1 Q1S)
US-09-948-391A-13

Query Match 99.1%; Score 573; DB 11; Length 105;
Best Local Similarity 100.0%; Pred. No. 3.7e-58;
Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFYISRPPEVKAICGIIASKNVLTT 61
Db 3 DWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFYISRPPEVKAICGIIASKNVLTT 62
Qy 62 EFYLSDCNVTSRPCKYKLLKKSNTNFCVTCENQAPVHFVGHC 104
Db 63 EFYLSDCNVTSRPCKYKLLKKSNTNFCVTCENQAPVHFVGHC 105

RESULT 10
US-09-961-400-13

Sequence 13, Application US/09961400
Publication No. US20030124131A1
GENERAL INFORMATION:
APPLICANT: RYBAK, SUSANNA M.
APPLICANT: GOLDENBERG, DAVID M.
APPLICANT: NEWTON, DIANNE L.
TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
CELLS
FILE REFERENCE: 018733/1059
CURRENT APPLICATION NUMBER: US/09/961,400
CURRENT FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: 09/622,613
PRIOR FILING DATE: 2000-08-17
PRIOR APPLICATION NUMBER: PCT/US99/06641
PRIOR FILING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: 60/079,751
PRIOR FILING DATE: 1998-03-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 13
LENGTH: 105
TYPE: PRF

ORGANISM: Rana pipiens
US-09-961-400-13

Query Match 99.1%; Score 573; DB 11; Length 105;
Best Local Similarity 100.0%; Pred. No. 3.7e-58;
Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFYISRPPEVKAICGIIASKNVLTT 61
Db 3 DWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFYISRPPEVKAICGIIASKNVLTT 62
Qy 62 EFYLSDCNVTSRPCKYKLLKKSNTNFCVTCENQAPVHFVGHC 104
Db 63 EFYLSDCNVTSRPCKYKLLKKSNTNFCVTCENQAPVHFVGHC 105

RESULT 11
US-09-948-391A-2

Sequence 2, Application US/09948391A
Publication No. US20030027311A1
GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: The United States of America
APPLICANT: as represented by The Secretary of the
Department of Health and Human Services
TITLE OF INVENTION: Recombinant Anti-Tumor RNase
FILE REFERENCE: 015280-343110US
CURRENT APPLICATION NUMBER: US/09/948,391A
CURRENT FILING DATE: 2002-05-10
PRIOR APPLICATION NUMBER: US 60/079,751
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: WO PCT/US99/06641
PRIOR FILING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: US 09/622,613
PRIOR FILING DATE: 2000-08-17
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 104
TYPE: PRF
ORGANISM: Rana pipiens
FEATURE:
OTHER INFORMATION: ribonuclease (RapiR1)
US-09-948-391A-2

Query Match 98.4%; Score 569; DB 11; Length 104;
Best Local Similarity 99.0%; Pred. No. 1.1e-57;
Matches 103; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QDWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFYISRPPEVKAICGIIASKNVLTT 60
Db 1 QDWLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFYISRPPEVKAICGIIASKNVLTT 60
Qy 61 SEFYLSDCNVTSRPCKYKLLKKSNTNFCVTCENQAPVHFVGHC 104
Db 61 SEFYLSDCNVTSRPCKYKLLKKSNTNFCVTCENQAPVHFVGHC 104

RESULT 12
US-09-948-391A-4

Sequence 4, Application US/09948391A
Publication No. US20030027311A1
GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: The United States of America
APPLICANT: as represented by The Secretary of the
Department of Health and Human Services
TITLE OF INVENTION: Recombinant Anti-Tumor RNase
FILE REFERENCE: 015280-343110US
CURRENT APPLICATION NUMBER: US/09/948,391A
CURRENT FILING DATE: 2002-05-10

PRIOR APPLICATION NUMBER: US 60/079, 751
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: WO PCT/US99/06641
PRIOR FILING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: US 09/622, 613
PRIOR FILING DATE: 2000-08-17
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4
LENGTH: 104
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Rana pipiens
OTHER INFORMATION: ribonuclease with Met231eu substitution
OTHER INFORMATION: (recombinant RapLRI Met231eu)
US-09-948-391A-4

Query Match 98.4%; Score 569; DB 11; Length 104;
Best Local Similarity 98.1%; Pred. No. 1,1e-57;
Matches 102; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QDWLTFQKHLTNTRDVCNNIMSTNLFHCKDKNTFIYSRPPVKAICKGIASKNVLT 60
DB 1 QDWLTFQKHLTNTRDVCNNIMSTNLFHCKDKNTFIYSRPPVKAICKGIASKNVLT 60
QY 61 SEFYISDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 104
DB 61 FEFYISDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 104

RESULT 13
US-09-961-400-4
Sequence 4, Application US/09961400
Publication No. US20030124131A1
GENERAL INFORMATION:
APPLICANT: RYBAK, SUSANNA M.
APPLICANT: GOLDBERG, DAVID M.
TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
TITLE OF INVENTION: CELLS
FILE REFERENCE: 018733/1059
CURRENT APPLICATION NUMBER: US/09/961,400
CURRENT FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: 09/622, 613
PRIOR FILING DATE: 2000-08-17
PRIOR APPLICATION NUMBER: PCT/US99/06641
PRIOR FILING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: 60/079, 751
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 104
TYPE: PRT
ORGANISM: Rana pipiens
US-09-961-400-4

Query Match 98.4%; Score 569; DB 11; Length 104;
Best Local Similarity 98.1%; Pred. No. 1,1e-57;
Matches 102; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QDWLTFQKHLTNTRDVCNNIMSTNLFHCKDKNTFIYSRPPVKAICKGIASKNVLT 60
DB 1 QDWLTFQKHLTNTRDVCNNIMSTNLFHCKDKNTFIYSRPPVKAICKGIASKNVLT 60
QY 61 SEFYISDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 104
DB 61 FEFYISDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 104

RESULT 14
US-09-961-400-8

Sequence 8, Application US/09961400
Publication No. US20030124131A1
GENERAL INFORMATION:
APPLICANT: RYBAK, SUSANNA M.
APPLICANT: GOLDBERG, DAVID M.
TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
TITLE OF INVENTION: CELLS
FILE REFERENCE: 018733/1059
CURRENT APPLICATION NUMBER: US/09/961,400
CURRENT FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: 09/622, 613
PRIOR FILING DATE: 2000-08-17
PRIOR APPLICATION NUMBER: PCT/US99/06641
PRIOR FILING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: 60/079, 751
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 8
LENGTH: 105
TYPE: PRT
ORGANISM: Rana pipiens
US-09-961-400-8

Query Match 97.8%; Score 565; DB 11; Length 105;
Best Local Similarity 97.1%; Pred. No. 3,1e-57;
Matches 101; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QDWLTFQKHLTNTRDVCNNIMSTNLFHCKDKNTFIYSRPPVKAICKGIASKNVLT 60
DB 2 QDWLTFQKHLTNTRDVCNNIMSTNLFHCKDKNTFIYSRPPVKAICKGIASKNVLT 61
QY 61 SEFYISDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 104
DB 62 FEFYISDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 105

RESULT 15
US-09-948-391A-8
Sequence 8, Application US/09948391A
Publication No. US20030027311A1
GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: The United States of America
APPLICANT: as represented by The Secretary of the
Department of Health and Human Services
TITLE OF INVENTION: Recombinant Anti-Tumor RNase
FILE REFERENCE: 015280-143110US
CURRENT APPLICATION NUMBER: US/09/948, 391A
CURRENT FILING DATE: 2002-05-10
PRIOR APPLICATION NUMBER: US 60/079, 751
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: WO PCT/US99/06641
PRIOR FILING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: US 09/622, 613
PRIOR FILING DATE: 2000-08-17
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 8
LENGTH: 105
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Rana pipiens
OTHER INFORMATION: ribonuclease with Met at position 1 and Met231eu
OTHER INFORMATION: substitution (recombinant Met(-1) RapLRI Met231eu)
US-09-948-391A-8

Query Match 96.9%; Score 560; DB 11; Length 105;
Best Local Similarity 97.1%; Pred. No. 1,2e-56;
Matches 101; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 ODLTFQKHLLNTRDVCNNIMSTNLFHCKDKNTEIYSRPEPVKAI CKGIASKVLT 60
DB 2 ODLTFQKHLLNTRDVCNNILSTNLFHCKDKNTEIYSRPEPVKAI CKGIASKVLT 61
OY 61 SEFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 104
DB 62 SEFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 105

Search completed: January 22, 2004, 12:12:25
Job time : 25.7341 secs

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OM protein - protein search, using sw model

Run on: January 22, 2004, 12:01:21 ; Search time 25.7079 Seconds

(without alignments)
1043.940 Million cell updates/sec

Title: US-09-622-613C-2

Sequence: 578

Scoring table: 1 QDMLTFQKHLTNRDVDCN.....TFCVTCEQAPVHFVGVGHC 104

Scoring table: Gapop 10.0, Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: SPTRMBL_23:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mammal:*
8: sp_mmc:*
9: sp_organelle:*
10: sp_phase:*
11: sp_plant:*
12: sp_rodent:*
13: sp_virus:*
14: sp_vertebrate:*
15: sp_unclassified:*
16: sp_rviro:*
17: sp_bacteriophage:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	578	100.0	127	0918V8	0918V8 rana pipien
2	556	96.2	127	08UYX5	08UYX5 rana pipien
3	404.5	70.0	129	09DFY6	09DFY6 rana pipien
4	386	66.8	128	09DFY8	09DFY8 rana pipien
5	311	53.8	128	09DFY7	09DFY7 rana pipien
6	309	53.5	128	09DFY5	09DFY5 rana pipien
7	298	51.6	133	098SM0	098SM0 rana pipien
8	292	50.5	133	098SM1	098SM1 rana pipien
9	286	49.5	133	098SM2	098SM2 rana pipien
10	282	48.8	133	098SM3	098SM3 rana pipien
11	280	48.4	132	098SM4	098SM4 rana pipien
12	275.5	47.7	132	09DF78	09DF78 rana pipien
13	157.5	27.2	129	09W738	09W738 xenopus lae
14	129	22.3	152	09UK15	09UK15 mus saxicol
15	127	22.0	157	09UK19	09UK19 meriones un

17	126.5	21.9	153	11	09UK17	09UK17 mus saxicol
18	126	21.8	157	11	09UK13	09UK13 meriones un
19	125	21.6	157	11	09UK14	09UK14 meriones un
20	123	21.3	154	11	09UK18	09UK18 mus saxicol
21	122	21.1	157	11	09UK01	09UK01 meriones un
22	121	20.9	157	11	09UK02	09UK02 meriones un
23	120.5	20.8	155	11	09UK09	09UK09 mus pahari
24	119.5	20.7	155	11	09UK13	09UK13 mus saxicol
25	116.5	20.2	155	11	09UK16	09UK16 mus saxicol
26	115.5	20.0	132	6	09TV25	09TV25 eulemur ful
27	115.5	20.0	155	11	09UK12	09UK12 mus saxicol
28	115.5	20.0	155	11	09UK14	09UK14 mus saxicol
29	114.5	19.8	170	6	09BE01	09BE01 ceratopithec
30	113.5	19.6	119	6	09TS06	09TS06 ceratopithec
31	113.5	19.6	119	6	09TV32	09TV32 gorilla gor
32	113.5	19.6	132	6	09TV24	09TV24 galago mono
33	113.5	19.6	147	6	08H200	08H200 pan troglod
34	113.5	19.6	155	11	09UK14	09UK14 ratus norv
35	113	19.6	156	11	09UK06	09UK06 mus caroli
36	113	19.6	156	11	09UK07	09UK07 mus caroli
37	112.5	19.5	119	6	09TV30	09TV30 saquinus oe
38	112.5	19.5	155	11	09UK125	09UK125 mus musculu
39	112.5	19.5	155	11	09UK08	09UK08 mus pahari
40	112	19.4	124	6	09TSF2	09TSF2 bos taurus
41	112	19.4	156	11	09UK07	09UK07 mus caroli
42	111.5	19.3	155	11	09UK03	09UK03 mus caroli
43	111	19.2	124	6	09SNG6	09SNG6 bubalus bub
44	111	19.2	156	6	08S004	08S004 lemur catla
45	111	19.2	156	11	09UK04	09UK04 mus caroli

ALIGNMENTS

RESULT 1
ID 0918V8 PRELIMINARY; PRT; 127 AA.

AC 0918V8: 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Onconase variant rapLRI precursor.
DS Rana pipiens (Northern leopard frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
CC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.
OX NCBI_TaxID=8404;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=20330357; PubMed=10871370;
RA Chen S.-L., Le S.-Y., Newton D.L., Maizel J.V. Jr., Rybak S.M.;
RT "A gender-specific mRNA encoding a cytotoxic ribonuclease contains a
3' UTR of unusual length and structure."
RL Nucleic Acids Res. 28:2375-2382(2000).
DR EMBL; AF165133; AAF76935.1; -;
DR HSSP; P22069; IONC.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; RNaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_Pc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW SIGNAL.
FT SIGNAL.
SQ SEQUENCE 127 AA; 14491 MW; B8511DC5407AB69B CRC64;

Query Match 100.0%; Score 578; DB 13; Length 127;
Best Local Similarity 100.0%; Pred. No. 4.3e-58;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QDMLTFQKHLTNRDVDCNIMSTULFCKDKNTFYSPPEPVKAICKGIASKVLT 60
DB 24 QDMLTFQKHLTNRDVDCNIMSTULFCKDKNTFYSPPEPVKAICKGIASKVLT 83

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OY 61 SEFYISDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFGVGH 104
DB 84 SEFYISDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFGVGH 127

RESULT 2
OY 08UVX5 PRELIMINARY; PRT: 127 AA.
AC Q8UVX5;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DR 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Oncocase precursor.
GN RPR.
OS Rana pipiens (Northern leopard frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Rana;
OX NCBI_TaxID=8404;
RN [1]
RP SEQUENCE FROM N.A.
RA Liao Y.-D., Wang S.-C.;
RT "Rana pipiens onconase genomic DNA.";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF332139; AAL54383.1; -.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; RNaseA. 1.
DR ProDom: PDD00535; RNaseA. 1.
DR SMART; SM00092; RNase_Pc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL.
SQ SEQUENCE 127 AA; 14469 MW; 953F90D351CFEEF3 CRC64;

Query Match 96.2%; Score 556; DB 13; Length 127;
Best Local Similarity 96.2%; Pred. No. 1.4e-55;
Matches 100; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 ODMLTFOCKHLTNRDVCNNIMSTNLFPHCKDKNTFYSRPVPVAKICKGIASKNVLT 60
DB 24 ODMLTFOCKHLTNRDVCNNIMSTNLFPHCKDKNTFYSRPVPVAKICKGIASKNVLT 83

OY 61 SEFYISDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFGVGH 104
DB 84 SEFYISDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFGVGH 127

RESULT 3
OY 09DFY6 PRELIMINARY; PRT: 129 AA.
AC Q9DFY6;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)
DR 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Rana catesbeiana (Bull frog).
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Rana;
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=Liver;
RC MEDLINE=20512555; PubMed=11058105;
RA Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.;
RT "Purification and cloning of cytotoxic ribonucleases from Rana
catesbeiana (bullfrog).";
Nucleic Acids Res. 28:4097-4104 (2000).
RN [2]
RP SEQUENCE FROM N.A.
RA TISSUE=Liver;
RC MEDLINE=20512555; PubMed=11058105;
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RT Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF242555; AAG31441.2; -.
HSP; P22069; IONC.
```

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DR InterPro: IPR001427; RNaseA.
DR Pfam; PF00074; RNaseA. 1.
DR ProDom; PDD00535; RNaseA. 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL.
SQ SEQUENCE 129 AA; 14724 MW; 826A628B2B10ABDA CRC64;

Query Match 70.0%; Score 404.5; DB 13; Length 129;
Best Local Similarity 67.6%; Pred. No. 2.5e-38;
Matches 71; Conservative 16; Mismatches 17; Indels 1; Gaps 1;

OY 1 ODMLTFOCKHLTNRDVCNNIMSTNLFPHCKDKNTFYSRPVPVAKICKGIASKNVLT 60
DB 24 ODMLTFOCKHLTNRDVCNNIMSTNLFPHCKDKNTFYSLQPVKALCRGVLFSAVLN 83

OY 61 SEFYISDCNVTSR--PCKYKLLKSTNTFCVTCENQAPVHFGVGH 104
DB 84 SEFYISDCNVTSRPCKYKLLKSSNRTICRCEHELVPVAFVAGVIG 128

RESULT 4
OY 09DFY8 PRELIMINARY; PRT: 128 AA.
AC Q9DFY8;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DR 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE R-RNase2 ribonuclease precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Rana;
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=Liver;
RC MEDLINE=20512555; PubMed=11058105;
RA Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.;
RT "Purification and cloning of cytotoxic ribonucleases from Rana
catesbeiana (bullfrog).";
Nucleic Acids Res. 28:4097-4104 (2000).
RN [2]
RP SEQUENCE FROM N.A.
RA TISSUE=Liver;
RC MEDLINE=20512555; PubMed=11058105;
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RT Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF242553; AAG31439.1; -.
DR HSP; P22069; IONC.
DR InterPro: IPR001427; RNaseA.
DR Pfam; PF00074; RNaseA. 1.
DR ProDom; PDD00535; RNaseA. 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL.
SQ SEQUENCE 128 AA; 14839 MW; 989719CF52053ECC CRC64;

Query Match 66.8%; Score 386; DB 13; Length 128;
Best Local Similarity 67.3%; Pred. No. 3.1e-36;
Matches 70; Conservative 10; Mismatches 24; Indels 0; Gaps 0;

OY 1 ODMLTFOCKHLTNRDVCNNIMSTNLFPHCKDKNTFYSRPVPVAKICKGIASKNVLT 60
DB 24 ODMLTFOCKHLTNRDVCNNIMSTNLFPHCKDKNTFYARPRVQALCKNIIVISKNVLT 83

OY 61 SEFYISDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFGVGH 104
DB 84 DEFYISDCNRIKLPCHYKLLKSSNTICITCENKLPVHVAVAVBEC 127

RESULT 5
OY 09DFY7
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ID Q9DFY7 PRELIMINARY; PRT; 128 AA.
AC Q9DFY7;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE RC-RNase3 ribonuclease precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_Taxid=8400;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=20512555; Pubmed=11058105;
RA Liao Y.-D., Huang H.-C., Liao Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RT "Purification and cloning of cytotoxic ribonucleases from Rana
RL catesbeiana (bullfrog).";
RL Nucleic Acids Res. 28:4097-4104(2000).
DR HSSP; P22069; 10NC.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL.
FT CHAIN 24 128 RC-RNASE3 RIBONUCLEASE.
SQ SEQUENCE 128 AA; 14517 MW; 281498082E0587D CRC64;

Query Match 53.8%; Score 311; DB 13; Length 128;
Best Local Similarity 54.8%; Pred. No. 1,1e-27;
Matches 57; Conservative 12; Mismatches 35; Indels 0; Gaps 0;

QY 1 QDMLTFOQKHLTNRDVCNNIMSTNLFHCKDKNTFYSRPEPVKAICKGIASKNVLT 60
DB 24 QDMETFOQKHLTDYKVKVCDVEMKALFDCKKNTFTFYALGVRVKAICKNIKDNITVLSR 83
QY 61 SEFYLSDCNVTSPCKYKLLKSTNTFCVTCENQAPVHFVGHC 104
DB 84 DVFYLPQCKNRKGLPCHYRLDGSNTTICLTCKELPIHFAGVGSC 127

RESULT 6
Q9DFY5 PRELIMINARY; PRT; 128 AA.
AC Q9DFY5;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE RC-RNasee ribonuclease precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_Taxid=8400;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=20512555; Pubmed=11058105;
RA Liao Y.-D., Huang H.-C., Liao Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RT "Purification and cloning of cytotoxic ribonucleases from Rana
RL catesbeiana (bullfrog).";
RL Nucleic Acids Res. 28:4097-4104(2000).
DR HSSP; P22069; 10NC.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.

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KW Signal.
FT SIGNAL.
FT CHAIN 24 128 RC-RNASE6 RIBONUCLEASE.
SQ SEQUENCE 128 AA; 14804 MW; AFE8FD67D266C7C2 CRC64;

Query Match 53.5%; Score 309; DB 13; Length 128;
Best Local Similarity 53.8%; Pred. No. 1,1e-27;
Matches 56; Conservative 13; Mismatches 35; Indels 0; Gaps 0;

QY 1 QDMLTFOQKHLTNRDVCNNIMSTNLFHCKDKNTFYSRPEPVKAICKGIASKNVLT 60
DB 24 QDMETFOQKHLTDYKVKVCDVEMKALFDCKKNTFTFYALGVRVKAICKNIKDNITVLSR 83
QY 61 SEFYLSDCNVTSPCKYKLLKSTNTFCVTCENQAPVHFVGHC 104
DB 84 DVFYLPQCKNRKGLPCHYRLDGSNTTICLTCKELPIHFAGVGKC 127

RESULT 7
Q98SMO PRELIMINARY; PRT; 133 AA.
AC Q98SMO;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE RNase A-type ribonuclease rc208 precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_Taxid=8400;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21539506; Pubmed=11683320;
RA Rosenbery H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT "Rapid diversification of RNase A superfamily ribonuclease from the
RL bullfrog, Rana catesbeiana.";
RL J. Mol. Evol. 53:31-38(2001).
DR EMBL; AF351209; AAK30255.1; -.
DR HSSP; P11916; 1BC4.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaaseA; 1.
DR PROSITE; PS000535; RNaseA; 1.
DR SMART; SM00092; RNase_Pc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL.
FT SEQUENCE 133 AA; 14628 MW; 87FCF122C3499E02 CRC64;

Query Match 51.6%; Score 298; DB 13; Length 133;
Best Local Similarity 49.5%; Pred. No. 3,4e-26;
Matches 55; Conservative 16; Mismatches 32; Indels 8; Gaps 3;

QY 1 QDMLTFOQKHLTNRDVCNNIMSTNLFHCKDKNTFYSRPEPVKAICKGIASKNV 56
DB 23 QNWTFOQKHITNTSSINCNTIMDNNTIYIGGCKGNTFTISSATVKAICTGVI 81
QY 57 VLTSEFYLSDC--NVTSPCKYKLLKSTNTFCVTCENQAPVHFVGHC 104
DB 82 VLTSTFOQKHLTNRDVCNNIMSTNLFHCKDKNTFYSRPEPVKAICKGIASKNV 132

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RESULT 8
Q9PMR7 PRELIMINARY; PRT; 133 AA.
AC Q9PMR7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Ribonuclease precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.

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RL J. Mol. Evol. 53:31-38(2001).
DR EMBL: AF51211; AAK30257.1;
DR HSSP; P11916; 1BC4.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; RNaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_Pc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL.
SQ SEQUENCE 133 AA; 14590 MW; 8B40B9A94FA5B943 CRC64;
Query Match 48.8%; Score 282; DB 13; Length 133;
Best Local Similarity 46.8%; Pred. No. 2.3e-24;
Matches 52; Conservative 18; Mismatches 33; Indels 8; Gaps 3;

OY 1 ODMLTFOKHLNTRVDNCCNMISTNLF---HCKDKNTFYISREPPVKAICKGIASKN 56
DB 23 QNMATFOBOHITNTSSINMNSLYIVGQCKKVTFFIASATVKGICSG-VTDKK 81
OY 57 VLTSEFYLSDC---VTSRPCKYKLKSTNTFCVTCENQAPVHPVGVGHC 104
DB 82 VLSTTFQLDICTRIFFITRPCCPYSSRTETNYICVCKENQYVHPVAGIGQC 132

RESULT 12
O98SM1 PRELIMINARY; PRT; 132 AA.
ID O98SM1;
AC O98SM1;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE RNase A-type ribonuclease rc204 precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP MEDLINE=21539506; Pubmed=11683320;
RA Rosenbery H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT "Rapid diversification of RNase A superfamily ribonuclease from the
RL bullfrog, Rana catesbeiana.";
RL J. Mol. Evol. 53:31-38(2001).
DR EMBL; AF51208; AAK30254.1;
DR HSSP; P11916; 1BC4.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; RNaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_Pc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL.
SQ SEQUENCE 132 AA; 14704 MW; 95061760F729868E CRC64;
Query Match 48.4%; Score 280; DB 13; Length 132;
Best Local Similarity 46.6%; Pred. No. 3.8e-24;
Matches 54; Conservative 14; Mismatches 35; Indels 8; Gaps 3;

OY 1 ODMLTFOKHLNTRVDNCCNMISTNLF---HCKDKNTFYISREPPVKAICKGIASKN 56
DB 23 QDMPTFOCKHLPSTSSIDCNTIMDKAIYIVGQCKKVTFFIYSATVKAICTGVLAN-N 81
OY 57 VLTSEFYLSDC---VTSRPCKYKLKSTNTFCVTCENQAPVHPVGVGHC 104
DB 82 VLSTTRFQLKXXTRTFITSRPCPYSSRTETNYICVCKENQYVHPVAGIGKC 132

RESULT 13
O9DF78 PRELIMINARY; PRT; 132 AA.
AC O9DF78;
DT 01-MAR-2001 (TREMBLrel. 16, Created)

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DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE OC-RNaseA1 ribonuclease precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP MEDLINE=20512555; Pubmed=11058105;
RA Liao Y.-D., Huang H.-C., Liu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RT "Purification and cloning of cytotoxic ribonucleases from Rana
RL catesbeiana (bullfrog).";
RL Nucleic Acids Res. 28:4097-4104(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF288642; AAG30414.2;
DR HSSP; P11916; 1BC4.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; RNaseA; 1.
DR ProDom; PD000535; RNase_Pc; 1.
DR SMART; SM00092; RNase_Pc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL.
SQ SEQUENCE 132 AA; 14625 MW; D8D9A517452FBE53 CRC64;
Query Match 47.7%; Score 275.5; DB 13; Length 132;
Best Local Similarity 44.1%; Pred. No. 1.2e-23;
Matches 49; Conservative 19; Mismatches 36; Indels 7; Gaps 2;

OY 1 ODMLTFOKHLNTRVDNCCNMISTNLF---HCKDKNTFYISREPPVKAICKGIASKN 56
DB 22 QNMATFOCKHITNTSSIDCNTIMDKAIYIVGQCKKERTFFIISSDNVKACISGVSPRK 81
OY 57 VLTSEFYLSDC---VTSRPCKYKLKSTNTFCVTCENQAPVHPVGVGHC 104
DB 82 ELSTTSFLNLTNCIRDSITRPCCPYSPDNKKICVCKEQJLPHVHPVAGIGKC 132

RESULT 14
O9W738 PRELIMINARY; PRT; 169 AA.
ID O9W738;
AC O9W738;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE FRL2 protein.
GN FRL2.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP MEDLINE=96069863; Pubmed=7585965;
RA Kinoshita N., Minshull J., Kirschner M.W.;
RT "The identification of two novel ligands of the FGF receptor by a
RL yeast screening method and their activity in Xenopus development.";
RL Cell 83:621-630(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC KINOSHITA N., KIRSCHNER M.W.;
RA Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF159166; AAD41901.1;
DR HSSP; P00656; 1LSQ.
DR InterPro; IPR001427; RNaseA.

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PT New recombinant ribonucleases, used for killing target cells, e.g. for
PT treating cancers, viral infections or autoimmune diseases -
PS Claim 1; Page 55; 71pp; English.
XX
CC The present sequence is Rana pipiens liver ribonuclease (RaplR1)
CC protein. Carboxy terminal end of RaplR1 has a covalently bound
CC ligand binding moiety, which can be a LL2 antibody directed against
CC CD22 on cancerous B cells or human chorionic gonadotrophin (hCG)
CC effective against Kaposi's Sarcoma cells. Recombinant ribonucleases can
CC be expressed in bacteria without an N-terminal methionine due to the
CC presence of a signal peptide that is cleaved by bacteria. The soluble
CC expression of ribonuclease allows the proteins to be fused in-frame with
CC ligand binding moieties to form cytotoxic fusion proteins. They can be
CC used for treatment of cancer and autoimmune diseases.
CC
XX
SQ Sequence 104 AA;
Query Match 100.0%; Score 578; DB 20; Length 104;
Best Local Similarity 100.0%; Pred. No. 2,3e-62;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 QDMLTFQKXHLNTRDVCNNIMSTNLFPHCKDKNTFIYSRPEPVKAICKGIASKVLT 60
1 QDMLTFQKXHLNTRDVCNNIMSTNLFPHCKDKNTFIYSRPEPVKAICKGIASKVLT 60
DB 61 SEFYISDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 104
61 SEFYISDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 104
DB 61 SEFYISDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 104
RESULT 2
ID AAY28867 standard; Protein; 105 AA.
AC AAY28867;
XX
XX 25-JAN-2000 (first entry)
DT
XX
XX Recombinant Met(-1) RaplR1.
DE
XX
XX Recombinant Met(-1) Rana pipiens ribonuclease; RaplR1; CD22; RNase;
KW covalently bound; LL2 antibody; ligand binding moiety; cancerous B cell;
KW Kaposi's sarcoma; human chorionic gonadotrophin; hCG; signal peptide;
KW recombinant ribonuclease; cytotoxic fusion protein; cancer; frog;
KW autoimmune disease.
XX
XX Rana pipiens.
OS Synthetic.
OS
OS
FH Key Location/Qualifiers
FT Misc-difference 1 /note= "Met not found in wild type RaplR1"
FT
XX
XX WO950398-A2.
XX
XX 07-OCT-1999.
PD
XX
XX 26-MAR-1999; 99WO-US06641.
PF
XX
XX 27-MAR-1998; 98US-0079751.
PR
XX
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA
XX
XX Newton DL, Rybak SM;
PI
XX
XX WPI; 1999-610847/52.
DR N-PSDB; AA208126.
DR
XX
XX New recombinant ribonucleases, used for killing target cells, e.g. for
PT treating cancers, viral infections or autoimmune diseases -
XX
XX Claim 34; Page 57; 71pp; English.
PS

XX
CC The present sequence is a recombinant Rana pipiens ribonuclease (RaplR1)
CC protein with Met at position 1. Carboxy terminal end of recombinant
CC RaplR1 has a covalently bound ligand binding moiety, which can be a LL2
CC antibody directed against CD22 on cancerous B cells or human chorionic
CC gonadotrophin (hCG) effective against Kaposi's sarcoma cells. Recombinant
CC ribonucleases can be expressed in bacteria without an N-terminal
CC methionine due to the presence of a signal peptide that is cleaved by
CC bacteria. The soluble expression of ribonuclease allows the proteins to
CC be fused in-frame with ligand binding moieties to form cytotoxic fusion
CC proteins. They can be used for treatment of cancer and autoimmune
CC diseases.
CC
XX
SQ Sequence 105 AA;
Query Match 100.0%; Score 578; DB 20; Length 105;
Best Local Similarity 100.0%; Pred. No. 2,3e-62;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 QDMLTFQKXHLNTRDVCNNIMSTNLFPHCKDKNTFIYSRPEPVKAICKGIASKVLT 60
2 QDMLTFQKXHLNTRDVCNNIMSTNLFPHCKDKNTFIYSRPEPVKAICKGIASKVLT 61
DB 61 SEFYISDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 104
61 SEFYISDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 104
DB 62 SEFYISDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 105
RESULT 3
ID AAY28879 standard; Protein; 127 AA.
AC AAY28879;
XX
XX 25-JAN-2000 (first entry)
DT
XX
XX Rana pipiens Clone 5alb ribonuclease.
DE
XX
XX Rana pipiens ribonuclease Clone 5alb; RaplR1; covalently bound; RNase;
KW LL2 antibody; ligand binding moiety; CD22; cancerous B cell; onconase;
KW Kaposi's Sarcoma; human chorionic gonadotrophin; hCG; cancer;
KW recombinant ribonuclease; frog; signal peptide; cytotoxic fusion protein;
KW autoimmune disease.
XX
XX Rana pipiens.
OS
OS
OS
FH Key Location/Qualifiers
FT Peptide 1..23 /label= "Signal peptide"
FT /note= "Putative"
FT Protein 24..127 /label= "Rana pipiens_Clone_5alb_ribonuclease"
FT
XX
XX WO950398-A2.
XX
XX 07-OCT-1999.
PD
XX
XX 26-MAR-1999; 99WO-US06641.
PF
XX
XX 27-MAR-1998; 98US-0079751.
PR
XX
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA
XX
XX Newton DL, Rybak SM;
PI
XX
XX WPI; 1999-610847/52.
DR N-PSDB; AA208136.
DR
XX
XX New recombinant ribonucleases, used for killing target cells, e.g. for
PT treating cancers, viral infections or autoimmune diseases -
XX
XX Disclosure; Page 69; 71pp; English.
PS

CC The present sequence is a Rana pipiens Clone 5a1b ribonuclease (RaplR1).
CC It is encoded by Clone 5a1b cDNA obtained from Rana pipiens liver mRNA
CC library. It exhibits differences with Onconase (RTM) at amino acid
CC residues 11, 20, 85 and 103. Carboxy terminal end of RapR1 has a
CC covalently bound ligand binding moiety, which can be a L12 antibody
CC directed against CD22 on cancerous B cells or human chorionic
CC gonadotrophin (hCG) effective against Kaposi's Sarcoma cells. Recombinant
CC ribonucleases can be expressed in bacteria without an N-terminal
CC methionine due to the presence of a signal peptide that is cleaved by
CC bacteria. The soluble expression of ribonuclease allows the proteins to
CC be fused in-frame with ligand binding moieties to form cytotoxic fusion
CC proteins. They can be used for treatment of cancer and autoimmune
CC diseases.

CC Sequence 127 AA;

Query Match 100.0%; Score 578; DB 20; Length 127;

Best Local Similarity 100.0%; Pred. No. 2.9e-62;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QDWLTFQKHLTNTRDVDCNNIMSTNLFPHCKDKNTFIYSRPEPVKAICKGIASKNVLT 60
DB 24 QDWLTFQKHLTNTRDVCNNIMSTNLFPHCKDKNTFIYSRPEPVKAICKGIASKNVLT 83

OY 61 SEFYLSDCNVTSRPCKYKLLKKSTNTPCVTCENQAPVHFVGHC 104
DB 84 SEFYLSDCNVTSRPCKYKLLKKSTNTPCVTCENQAPVHFVGHC 127

RESULT 4

AAV28866
ID AAV28866 standard; Protein; 104 AA.

XX AAV28866;

DT 25-JAN-2000 (first entry)

XX Recombinant RapR1 Met23Leu amino acid sequence.

XX Recombinant Rana pipiens ribonuclease; RapR1 Met23Leu; covalently bound;
KM L12 antibody; ligand binding moiety; CD22; cancerous B cell; RNase;
KM Kaposi's sarcoma; human chorionic gonadotrophin; hCG; signal peptide;
KM recombinant ribonuclease; cytotoxic fusion protein; cancer; frog;
KM autoimmune disease.

XX Rana pipiens.
OS Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 23 /note= "Wild type Met replaced with Leu"

XX MO9950398-A2.

XX 07-OCT-1999.

XX 26-MAR-1999; 99WO-US06641.

XX 27-MAR-1998; 98US-0079751.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Newton DL, Rybak SM;

XX MPI; 1999-610847/52.

XX N-PSDB; AA208125.

XX New recombinant ribonucleases, used for killing target cells, e.g. for
PT treating cancers, viral infections or autoimmune diseases -
XX Claim 34; Page 56; 71pp; English.

XX The present sequence is a recombinant Rana pipiens ribonuclease (RaplR1)

CC protein with Met23Leu. Carboxy terminal end of recombinant RapR1 has a
CC covalently bound ligand binding moiety, which can be a L12 antibody
CC directed against CD22 on cancerous B cells or human chorionic
CC gonadotrophin (hCG) effective against Kaposi's sarcoma cells. Recombinant
CC ribonucleases can be expressed in bacteria without an N-terminal
CC methionine due to the presence of a signal peptide that is cleaved by
CC bacteria. The soluble expression of ribonuclease allows the proteins to
CC be fused in-frame with ligand binding moieties to form cytotoxic fusion
CC proteins. They can be used for treatment of cancer and autoimmune
CC diseases.

CC Sequence 104 AA;

Query Match 99.5%; Score 575; DB 20; Length 104;

Best Local Similarity 99.0%; Pred. No. 5.3e-62;
Matches 103; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QDWLTFQKHLTNTRDVDCNNIMSTNLFPHCKDKNTFIYSRPEPVKAICKGIASKNVLT 60
DB 1 QDWLTFQKHLTNTRDVCNNIMSTNLFPHCKDKNTFIYSRPEPVKAICKGIASKNVLT 60

OY 61 SEFYLSDCNVTSRPCKYKLLKKSTNTPCVTCENQAPVHFVGHC 104
DB 61 SEFYLSDCNVTSRPCKYKLLKKSTNTPCVTCENQAPVHFVGHC 104

RESULT 5

AAV28869
ID AAV28869 standard; Protein; 105 AA.

XX AAV28869;

DT 25-JAN-2000 (first entry)

XX Recombinant Met(-1) RapR1 Met23Leu-(His)6 protein.

XX Recombinant Met(-1) Rana pipiens ribonuclease Met23Leu-(His)6; RapR1;
KM CD22; covalently bound; L12 antibody; ligand binding moiety; RNase;
KM cancerous B cell; Kaposi's sarcoma; human chorionic gonadotrophin; hCG;
KM signal peptide; recombinant ribonuclease; cytotoxic fusion protein;
KM cancer; frog; autoimmune disease.

XX Rana pipiens.
OS Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 1 /note= "(His)6 histidine tag attached to N-terminal Met"

FT Misc-difference 1 /note= "Met not found in wild type RapR1"

FT Misc-difference 24 /note= "Wild type Met replaced with Leu"

XX MO9950398-A2.

XX 07-OCT-1999.

XX 26-MAR-1999; 99WO-US06641.

XX 27-MAR-1998; 98US-0079751.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Newton DL, Rybak SM;

XX MPI; 1999-610847/52.

XX N-PSDB; AA208127.

XX New recombinant ribonucleases, used for killing target cells, e.g. for
PT treating cancers, viral infections or autoimmune diseases -
XX Claim 4; Page 59; 71pp; English.

CC The present sequence is a recombinant Rana pipiens ribonuclease protein
CC (RaplR1) with Met at position 1 attached to (His)6 tag and Met24Leu.
CC Carboxy terminal end of recombinant RapLr1 has a covalently bound ligand
CC binding moiety, which can be a Ll2 antibody directed against CD22 on
CC cancerous B cells or human chorionic gonadotrophin (hCG) effective
CC against Kaposi's sarcoma cells. Recombinant ribonucleases can be
CC expressed in bacteria without an N-terminal methionine due to the
CC presence of a signal peptide that is cleaved by bacteria. The soluble
CC expression of ribonuclease allows the proteins to be fused in-frame with
CC ligand binding moieties to form cytotoxic fusion proteins. They can be
CC used for treatment of cancer and autoimmune diseases.

XX Sequence 105 AA;

Query Match 99.5%; Score 575; DB 20; Length 105;
Best Local Similarity 99.0%; Pred. No. 5,3e-62;

Matches 103; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Dy 1 QDMLTFQKKHLNTRDVCNNIMSTNLFPHCKDKNTFIYSRPPVKAICGIIASKVLT 60
2 QDMLTFQKKHLNTRDVCNNIMSTNLFPHCKDKNTFIYSRPPVKAICGIIASKVLT 61
61 SEFYLSDCNVTSRPCKYKLLKSKSTNTFCVTCENQAPVHFVGCHC 104
62 SEFYLSDCNVTSRPCKYKLLKSKSTNTFCVTCENQAPVHFVGCHC 105
Db

RESULT 6

AA28870
ID AAY28870 standard; Protein; 104 AA.

XX AAY28870;

DT 25-JAN-2000 (first entry)

XX Recombinant RapLr1 GlnSer amino acid sequence.

XX Recombinant Rana pipiens ribonuclease; RapLr1 GlnSer; covalently bound;
KW Ll2 antibody; ligand binding moiety; CD22; cancerous B cell; frog;
KW Kaposi's sarcoma; human chorionic gonadotrophin; hCG; signal peptide;
KW recombinant ribonuclease; cytotoxic fusion protein; cancer; RNase;
KW autoimmune disease.

OS Rana pipiens.
OS Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 1 /note= "Wild type Gln replaced with Ser"

XX MO9950398-A2.

XX 07-OCT-1999.

XX 26-MAR-1999; 99WO-US06641.

XX 27-MAR-1998; 98US-0079751.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Newton DL, Rybak SM;

XX MPI: 1999-610847/52.

XX N-PSDB; AA208128.

XX New recombinant ribonucleases, used for killing target cells, e.g. for
PT treating cancers, viral infections or autoimmune diseases -

XX Claim 34; Page 60; 71pp; English.

XX The present sequence is a recombinant Rana pipiens ribonuclease (RaplR1)
CC protein with GlnSer. Carboxy terminal end of recombinant RapLr1 has a
CC covalently bound ligand binding moiety, which can be a Ll2 antibody

CC directed against CD22 on cancerous B cells or human chorionic
CC gonadotrophin (hCG) effective against Kaposi's sarcoma cells. Recombinant
CC ribonucleases can be expressed in bacteria without an N-terminal
CC methionine due to the presence of a signal peptide that is cleaved by
CC bacteria. The soluble expression of ribonuclease allows the proteins to
CC be fused in-frame with ligand binding moieties to form cytotoxic fusion
CC proteins. They can be used for treatment of cancer and autoimmune
CC diseases.

XX Sequence 104 AA;

Query Match 99.1%; Score 573; DB 20; Length 104;
Best Local Similarity 100.0%; Pred. No. 9,2e-62;

Matches 103; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Dy 2 DMLTFQKKHLNTRDVCNNIMSTNLFPHCKDKNTFIYSRPPVKAICGIIASKVLT 61
2 DMLTFQKKHLNTRDVCNNIMSTNLFPHCKDKNTFIYSRPPVKAICGIIASKVLT 61
62 EPHYLSDCNVTSRPCKYKLLKSKSTNTFCVTCENQAPVHFVGCHC 104
62 EPHYLSDCNVTSRPCKYKLLKSKSTNTFCVTCENQAPVHFVGCHC 104
Db

RESULT 7

AA28871
ID AAY28871 standard; Protein; 105 AA.

XX AAY28871;

DT 25-JAN-2000 (first entry)

XX Recombinant Met(-1) RapLr1 GlnSer amino acid sequence.

XX Recombinant Met(-1) Rana pipiens ribonuclease GlnSer; RapLr1; CD22;
KW covalently bound; Ll2 antibody; ligand binding moiety; cancerous B cell;
KW Kaposi's sarcoma; human chorionic gonadotrophin; hCG; signal peptide;
KW recombinant ribonuclease; cytotoxic fusion protein; cancer; frog;
KW autoimmune disease; RNase.

OS Rana pipiens.
OS Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 1 /note= "Met not found in wild type RapLr1"

FT Misc-difference 2 /note= "Wild type Gln replaced with Ser"

XX MO9950398-A2.

XX 07-OCT-1999.

XX 26-MAR-1999; 99WO-US06641.

XX 27-MAR-1998; 98US-0079751.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Newton DL, Rybak SM;

XX MPI: 1999-610847/52.

XX N-PSDB; AA208129.

XX New recombinant ribonucleases, used for killing target cells, e.g. for
PT treating cancers, viral infections or autoimmune diseases -

XX Claim 34; Page 61; 71pp; English.

XX The present sequence is a recombinant Rana pipiens ribonuclease (RaplR1)
CC protein with Met at position 1 and GlnSer. Carboxy terminal end of
CC recombinant RapLr1 has a covalently bound ligand binding moiety, which
CC can be a Ll2 antibody directed against CD22 on cancerous B cells or human

DE Amino acid sequence of a frog ribonuclease protein.
 XX
 KW Frog; ribonuclease; rarnprimase; RNase.
 XX
 OS Rana pipiens.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1 /note="this Gln is autocyclised to pyroglutamic acid"
 XX
 XX
 PN US6175003-B1.
 PD 16-JAN-2001.
 XX
 XX 10-SEP-1999; 99US-0394268.
 XX
 XX 10-SEP-1999; 99US-0394268.
 PR 10-SEP-1999; 99US-0394268.
 XX
 XX (ALFA-) ALFACELL CORP.
 PA
 XX Saxena SK;
 PI
 XX MPI; 2001-167808/17.
 DR
 XX
 XX
 PT New nucleic acids encoding a ribonuclease (RNase), useful for the
 PT precise targeting of RNase to a predetermined cell receptor -
 XX
 XX
 PS Claim 1; Columns 5-6; 7pp; English.
 XX
 XX The present sequence represents a frog ribonuclease protein (rarnprimase)
 CC (RNase). The specification describes a synthetic ribonuclease protein,
 CC in which the addition of cysteine in the ribonuclease facilitates the
 CC chemical linking of a targeting molecule by the single reactive
 CC sulfhydryl group. The specification also describes a method for the
 CC production of rarnprimase using DNA technology instead of processing
 CC biological material. The re-engineering of the protein molecule allows
 CC easier attachment to a targeting molecule thereby making it possible for
 CC the ribonuclease to be delivered to a particular cell receptor where it
 CC might be most effective.
 CC
 XX
 SQ Sequence 104 AA;
 XX
 XX
 XX Query Match 96.2%; Score 556; DB 22; Length 104;
 XX Best Local Similarity 96.2%; Pred. No. 1.1e-59;
 XX Matches 100; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 XX
 QY 1 QDWLTFQKXGLNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAIKGIISKVLT 60
 XX
 DB 1 QDWLTFQKXGLNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAIKGIISKVLT 60
 XX
 QY 61 SEFYLSDCNVTSPCKYKLLKKSNTFCVCENAPVHFVGVGHC 104
 XX
 DB 61 SEFYLSDCNVTSPCKYKLLKKSNTFCVCENAPVHFVGVGSC 104
 XX
 XX
 XX RESULT 11
 XX ABG32650
 ID ABG32650 standard; Protein; 104 AA.
 XX
 XX ABG32650;
 XX
 XX 15-NOV-2002 (first entry)
 XX
 XX Northern leopard frog rarnprimase protein.
 DE
 XX Northern leopard frog rarnprimase protein.
 XX
 XX Northern leopard frog; rarnprimase; site-directed mutation; ribonuclease.
 XX
 XX Rana pipiens.
 OS
 XX US6423515-B1.
 PN
 XX 23-JUL-2002.
 PD
 XX

PF 14-OCT-2000; 2000US-0687748.
 XX
 XX 10-SEP-1999; 99US-0394268.
 XX
 XX (ALFA-) ALFACELL CORP.
 PA
 XX Saxena SK;
 PI
 XX MPI; 2002-664633/71.
 DR
 XX
 XX
 XX Constructing isolated nucleic acid encoding ribonuclease, by subjecting
 PT desired recombinant plasmid DNA to different site-directed mutations to
 PT produce nucleic acid, using different polymerase chain reaction
 PT protocols -
 XX
 XX
 XX Claim 1; Column 5-6; 8pp; English.
 PS
 XX The present invention relates to a new method of constructing isolated
 CC nucleic acid encoding ribonuclease protein with N-terminal Met at
 CC position -1 and Glu at position 1, where its Met has been cleaved and
 CC its Glu has been autocyclised. The method of the invention involves
 CC subfecting pET10d-rnc(Q1,W23L) plasmid DNA to two different
 CC site-directed mutations, each using overlapping PCR protocol. The method
 CC is useful for constructing an isolated nucleic acid encoding the
 CC ribonuclease. The present amino acid sequence represents the northern
 CC leopard frog rarnprimase protein of the invention.
 CC
 XX
 SQ Sequence 104 AA;
 XX
 XX
 XX Query Match 96.2%; Score 556; DB 23; Length 104;
 XX Best Local Similarity 96.2%; Pred. No. 1.1e-59;
 XX Matches 100; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 XX
 QY 1 QDWLTFQKXGLNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAIKGIISKVLT 60
 XX
 DB 1 QDWLTFQKXGLNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAIKGIISKVLT 60
 XX
 QY 61 SEFYLSDCNVTSPCKYKLLKKSNTFCVCENAPVHFVGVGHC 104
 XX
 DB 61 SEFYLSDCNVTSPCKYKLLKKSNTFCVCENAPVHFVGVGSC 104
 XX
 XX
 XX RESULT 12
 XX AAW35126
 ID AAW35126 standard; Protein; 379 AA.
 XX
 XX AAW35126;
 XX
 XX 20-APR-1998 (first entry)
 XX
 XX R. pipiens recombinant RNase rnc fusion protein 2.
 DE
 XX RNase A; ribonuclease; cytotoxic; oncogene; nOnc; immunofusion;
 KW tumour cell growth; frog.
 XX
 XX Rana pipiens.
 OS
 XX Synthetic.
 OS
 XX WO9731116-A2.
 PN
 XX 28-AUG-1997.
 PD
 XX 19-FEB-1997; 97WO-US02588.
 XX
 XX 21-FEB-1996; 96US-0011800.
 PR
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PA
 XX Boque L, Newton DL, Rybak SM, Wlodawer A;
 PI MPI; 1997-435168/40.
 XX
 XX N-PSDB; AAT94964.
 DR
 XX

PT Ribonuclease molecules based on native Oncanase - used for killing
PT cells, particularly tumour cells
XX
PS Disclosure; Page 68; 90pp; English.
XX
CC Sequences AAW35125 to AAW35135 represent recombinant fusion proteins
CC (Ronc) which are modifications of the Rnase Oncanase (RNM) (Rnc). Such
CC novel ribonuclease molecules are highly cytotoxic and can be used alone
CC or to form chemical conjugates or to target recombinant immunofusions.
CC They are used particularly for decreasing tumour cell growth. They can
CC also be used for cell separation in vitro by selectively killing unwanted
CC types of cells, e.g. in bone marrow prior to transplantation into a
CC patient undergoing marrow ablation by radiation, or for killing leukaemia
CC cells or T-cells that would cause graft versus host disease. The toxins
CC can also be used to selectively kill unwanted cells in culture. The new
CC ribonucleases have increased cytotoxic activity compared to ronc and
CC also lower immunogenicity in humans.
XX
SQ Sequence 379 AA;

Query Match 96.2%; Score 556; DB 18; Length 379;
Best Local Similarity 96.2%; Pred. No. 5.7e-59;
Matches 100; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 ODMLTFQKXHLNTRDVCNNIMSTNLFPHCKDKNTFIYSRPPVPAICGIIASKVLT 60
DB 26 ODMLTFQKXHLNTRDVCNNIMSTNLFPHCKDKNTFIYSRPPVPAICGIIASKVLT 85
OY 61 SEFYISDCNVTSRPCKYKXKSTNTFCYTCENQAPVHFVGVGHC 104
DB 86 SEFYISDCNVTSRPCKYKXKSTNTFCYTCENQAPVHFVGVGSC 129

RESULT 13

AAR12344

ID AAR12344 standard; protein; 104 AA.

XX AAR12344;

XX 08-AUG-1991 (first entry)

XX Protein with activity against cancer cells.

XX Frog eggs; Tamoxifen; Stelazine; cancer.

XX Rana pipiens.

XX WO9107435-A.

XX 30-MAY-1991.

XX 26-OCT-1990; 90WO-US06185.

XX 18-MAY-1990; 90US-0526314.

XX 13-NOV-1989; 89US-0436141.

XX (ALFA-) ALFACELL CORP.

XX Ardelc WJ, Mikulski SM;

XX WPI; 1991-178059/24.

XX New protein from fertilised eggs of Rana pipiens - active against
XX cancer cells, esp. in combination with Tamoxifen or Stelazine
XX (trifluoro-per-azine).

XX Claim 7; Fig 2; 33pp; English.

XX The protein is derived from fertilised frog eggs. It has an iso-
XX electric point of 9.5 - 10.5, a blocked N-terminal gp. and is free
XX of carboxyhydrates. It is active against certain cancer cells. The
XX combination of the protein and (2-1-p-dimethylaminoethoxyphenyl)-1,
XX 2-diphenyl-1-butene) citrate salt (tamoxifen) is much more bio-

CC active than the separate entities against human pancreatic ASPC-1
CC adenocarcinoma, and the combination of protein and (10-[3-(4-methyl
CC piperazin-1-yl)-propyl]-2-trifluoromethylphenothiazine (Stelazine)
CC is much more reactive than the separate entities against human sub-
CC A-549 carcinoma. Activity has also been shown against human adeno-
CC carcinoma NIH-OVCAR-3 cells, human leukemic HL-60 cells, human
CC COLO 320 DM cells, human LOK melanoma and human lung squamous car-
CC cinoma HT-520 cells.
XX
SQ Sequence 104 AA;

Query Match 95.7%; Score 553; DB 12; Length 104;
Best Local Similarity 95.2%; Pred. No. 2.5e-59;
Matches 99; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 ODMLTFQKXHLNTRDVCNNIMSTNLFPHCKDKNTFIYSRPPVPAICGIIASKVLT 60
DB 1 EDMLTFQKXHLNTRDVCNNIMSTNLFPHCKDKNTFIYSRPPVPAICGIIASKVLT 60
OY 61 SEFYISDCNVTSRPCKYKXKSTNTFCYTCENQAPVHFVGVGHC 104
DB 61 SEFYISDCNVTSRPCKYKXKSTNTFCYTCENQAPVHFVGVGSC 104

RESULT 14

AAR47303

ID AAR47303 standard; protein; 104 AA.

XX AAR47303;

XX 25-MAR-2003 (updated)

XX 09-SEP-1994 (first entry)

XX ONCOMASE (pharmaceutical protein).

XX Oncanase; pharmaceutical; protein; adenocarcinoma; treatment;

XX cisplatin; melphalan; adriamycin; ovarian cancer; ovary.

XX Synthetic.

XX WO9403197-A1.

XX 17-FEB-1994.

XX 02-JUL-1993; 93WO-US06357.

XX 30-JUL-1992; 92US-0921180.

XX (ALFA-) ALFACELL CORP.

XX Ardelc WJ, Mikulski SM;

XX WPI; 1994-065396/08.

XX Pharmaceutical compy. Cisplatin, Melphalan or Adriamycin - active
XX in-vitro against OVCAR-3 human ovarian adenocarcinoma cells
XX
XX Claim 7; Page 13; 18pp; English.

XX This pharmaceutical protein (ONCOMASE) is used in the production of
XX a bioactive pharmaceutical composition also comprising one of
XX Cisplatin (cis-diamminedichloroplatinum), Melphalan, (4-(bis-(2-
XX chloroethyl)amino)-L-phenylamine) or Adriamycin (doxorubicin HCl).
XX The composition has bioactivity in vitro against OVCAR-3 human
XX ovarian adenocarcinoma cells.
XX (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 104 AA;

Query Match 95.7%; Score 553; DB 15; Length 104;
Best Local Similarity 95.2%; Pred. No. 2.5e-59;
Matches 99; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Search completed: January 22, 2004, 12:06:22
Job time : 33.7191 secs

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DB 1 EDWLTFQKXHLNTRDVCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIISKVLT 60
QY 61 SEFYLSDCNVTSRPCKYKLLKSTNFCVTCENQAPVHFVGVGHC 104
DB 61 SEFYLSDCNVTSRPCKYKLLKSTNFCVTCENQAPVHFVGVGSC 104

RESULT 15

AAW00736
ID AAW00736 standard; protein; 104 AA.

XX AAW00736;

DT 25-MAR-2003 (updated)
DT 22-MAY-1997 (first entry)

DE Protein derived from frogs eggs.

XX Rana pipiens; ovarian adenocarcinoma NIH-OVCAR03 cell; frog; egg;
KW submaxillary epidermoid carcinoma A-253 cell; tumour; human;
KM leukaemic HL-60 cell; COLO 320 DM cell; colon adenocarcinoma;
KM LOX melanoma; lung squamous carcinoma HT-520 cell.

XX Rana pipiens.

XX US5559212-A.

XX 24-SEP-1996.

XX 01-AUG-1994; 94US-0283970.

XX 03-FEB-1992; 92US-0814332.

XX 06-APR-1988; 88US-0178118.

XX 13-NOV-1989; 89US-0436141.

XX 01-AUG-1994; 94US-0283970.

XX (ALFA-) ALFACELL CORP.

XX Ardelc WJ;

XX WPI; 1996-442459/44.
XX New isolated Rana pipiens frog protein - useful for the treatment of
XX tumours.

XX Claim 1; Column 8; 7p; English.

XX This sequence represents a protein which was prepared by homogenisation
XX of Rana pipiens frogs eggs. This protein is used for treating tumours
XX in humans. Especially this protein was active against human
XX submaxillary epidermoid carcinoma A-253 cells, human ovarian
XX adenocarcinoma NIH-OVCAR03 cells, human leukaemic HL-60 cells, human
XX COLO 320 DM cells originally isolated from colon adenocarcinoma, human
XX LOX melanoma and human lung squamous carcinoma HT-520 cells.
XX (updated on 25-MAR-2003 to correct PF field.)

XX Sequence 104 AA;

Query Match 95.7%; Score 553; DB 17; Length 104;
Best Local Similarity 95.2%; Pred. No. 2.5e-59;
Matches 99; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 QDWLTFQKXHLNTRDVCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIISKVLT 60
DB 1 EDWLTFQKXHLNTRDVCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIISKVLT 60

QY 61 SEFYLSDCNVTSRPCKYKLLKSTNFCVTCENQAPVHFVGVGHC 104
DB 61 SEFYLSDCNVTSRPCKYKLLKSTNFCVTCENQAPVHFVGVGSC 104

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OM protein - protein search, using SW model

Run on: January 22, 2004, 12:01:30 ; Search time 12.4644 Seconds
(without alignments)
353.031 Million cell updates/sec

Title: US-09-622-613C-2

Perfect score: 578

Sequence: 1 QDWLTFQKHLTNTRVDGN.....TFCVTCENQAPVHVGVGHG 104

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Issued_Patents_AA.*
1: /cgn2_6/ptodata/1/iaa/5A.COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B.COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A.COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B.COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS.COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	558	96.5	104	1	US-08-467-955-2
2	556	96.2	104	3	US-09-394-268-1
3	556	96.2	104	4	US-09-687-748-1
4	556	96.2	129	3	US-08-875-811-63
5	556	96.2	129	3	US-08-875-811-43
6	553	95.7	104	1	US-08-283-971-1
7	553	95.7	104	1	US-07-921-619-1
8	553	95.7	104	1	US-08-467-955-1
9	553	95.7	104	2	US-08-891-848-13
10	553	95.7	105	3	US-08-875-811-39
11	553	95.7	105	3	US-08-875-811-41
12	553	95.7	104	3	US-08-875-811-51
13	551	95.3	104	3	US-08-875-811-1
14	551	95.3	104	4	US-09-071-672-1
15	551	95.3	106	3	US-08-875-811-28
16	551	95.3	107	3	US-08-875-811-30
17	551	95.3	112	3	US-08-875-811-32
18	551	95.3	121	3	US-08-875-811-59
19	551	95.3	254	3	US-08-875-811-61
20	551	95.3	355	3	US-08-875-811-49
21	551	95.3	355	3	US-08-875-811-57
22	551	95.3	355	3	US-08-875-811-64
23	551	95.3	366	3	US-08-875-811-55
24	548	94.8	104	4	US-09-394-268-2
25	546	94.5	105	3	US-09-687-748-2
26	546	94.5	105	3	US-08-875-811-24
27	546	94.5	105	3	US-08-875-811-26

28	542	93.8	358	3	US-08-875-811-45	Sequence 45, App1
29	542	93.8	365	3	US-08-875-811-53	Sequence 53, App1
30	527	91.2	107	3	US-08-875-811-20	Sequence 20, App1
31	490	84.8	360	3	US-08-875-811-47	Sequence 47, App1
32	483.5	83.7	111	3	US-08-875-811-22	Sequence 22, App1
33	445	77.0	83	3	US-08-875-811-2	Sequence 2, App1
34	445	77.0	83	4	US-09-071-672-3	Sequence 3, App1
35	289	50.0	111	2	US-08-891-848-12	Sequence 12, App1
36	289	50.0	111	3	US-08-875-811-8	Sequence 8, App1
37	217.5	37.6	114	3	US-09-223-118-4	Sequence 4, App1
38	205.5	35.6	114	3	US-09-223-118-2	Sequence 2, App1
39	204.5	35.4	114	3	US-09-223-118-1	Sequence 1, App1
40	202.5	35.0	114	3	US-09-223-118-3	Sequence 3, App1
41	157.5	27.2	169	1	US-08-441-629-2	Sequence 2, App1
42	157.5	27.2	169	3	US-08-776-207-2	Sequence 2, App1
43	157.5	27.2	169	4	US-09-507-773-2	Sequence 2, App1
44	157.5	27.2	169	5	PCT-US95-09172-2	Sequence 2, App1
45	146	25.3	28	3	US-08-875-811-3	Sequence 3, App1

ALIGNMENTS

RESULT 1
US-08-467-955-2
Sequence 2, Application US/08467955
Patent No. 5728805
GENERAL INFORMATION:
APPLICANT: Ardelit Ph.D., Wojciech J.
TITLE OF INVENTION: PHARMACEUTICALS AND METHOD FOR MAKING THEM
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Mark H. Jay, P.A.
STREET: P.O. Box E
CITY: Short Hills
STATE: New Jersey
COUNTRY: USA
ZIP: 07078-0383
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,955
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/178,118
FILING DATE: 06-APR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/436,141
FILING DATE: 13-NOV-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/814,332
FILING DATE: 03-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/283,970
FILING DATE: 01-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Jay, Mark H.
REGISTRATION NUMBER: 27507
REFERENCE/DOCKET NUMBER: 5007 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-912-9066
TELEFAX: 201-912-0442
TELEX: No. 5728805 Applicable
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 104 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: protein
HYPOTHETICAL: N
ANTI-SENSE: N
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Rana pipiens
DEVELOPMENTAL STAGE: Oocyte
US-08-467-955-2

Query Match 96.5%; Score 558; DB 1; Length 104;
Best Local Similarity 96.2%; Pred. No. 1.6e-60;
Matches 100; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ODMLTFQKKHLTNRDVCNNIMSTNLFPHCKDKNTFIYSRPPVKAICKGIASKNVLT 60
DB 1 EDMLTFQKKHLTNRDVCNNIMSTNLFPHCKDKNTFIYSRPPVKAICKGIASKNVLT 60
QY 61 SEFYISDCNVTSRPCKYKLLKSTNFCVTCENQAPVHFVGVGHC 104
DB 61 SEFYISDCNVTSRPCKYKLLKSTNFCVTCENQAPVHFVGVGRC 104

RESULT 2

US-09-394-268-1
Sequence 1, Application US/09394268
Patent No. 6175003
GENERAL INFORMATION:
APPLICANT: Saxena, Shailendra K
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING RIBONUCLEASES AND METHODS OF
TITLE OF INVENTION: MAKING THEM
FILE REFERENCE: 5013
CURRENT APPLICATION NUMBER: US/09/394,268
CURRENT FILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 104
TYPE: PRT
ORGANISM: Rana pipiens
US-09-394-268-1

Query Match 96.2%; Score 556; DB 3; Length 104;
Best Local Similarity 96.2%; Pred. No. 2.9e-60;
Matches 100; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ODMLTFQKKHLTNRDVCNNIMSTNLFPHCKDKNTFIYSRPPVKAICKGIASKNVLT 60
DB 1 ODMLTFQKKHLTNRDVCNNIMSTNLFPHCKDKNTFIYSRPPVKAICKGIASKNVLT 60
QY 61 SEFYISDCNVTSRPCKYKLLKSTNFCVTCENQAPVHFVGVGHC 104
DB 61 SEFYISDCNVTSRPCKYKLLKSTNFCVTCENQAPVHFVGVGSC 104

RESULT 3

US-09-687-748-1
Sequence 1, Application US/09687748
Patent No. 6423515
GENERAL INFORMATION:
APPLICANT: Saxena, Shailendra K
TITLE OF INVENTION: METHODS OF MAKING NUCLEIC ACIDS ENCODING RIBONUCLEASES
FILE REFERENCE: 5013 US 01
CURRENT APPLICATION NUMBER: US/09/687,748
CURRENT FILING DATE: 2000-10-14
PRIOR APPLICATION NUMBER: 09/394,268
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 104
TYPE: PRT
ORGANISM: Rana pipiens
US-09-687-748-1

Query Match 96.2%; Score 556; DB 4; Length 104;
Best Local Similarity 96.2%; Pred. No. 2.9e-60;
Matches 100; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ODMLTFQKKHLTNRDVCNNIMSTNLFPHCKDKNTFIYSRPPVKAICKGIASKNVLT 60
DB 1 ODMLTFQKKHLTNRDVCNNIMSTNLFPHCKDKNTFIYSRPPVKAICKGIASKNVLT 60
QY 61 SEFYISDCNVTSRPCKYKLLKSTNFCVTCENQAPVHFVGVGHC 104
DB 61 SEFYISDCNVTSRPCKYKLLKSTNFCVTCENQAPVHFVGVGSC 104

RESULT 4

US-08-875-811-63
Sequence 63, Application US/08875811
Patent No. 6045793
GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Boque, Lluís
APPLICANT: Wlodawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Paris, Susan K.
REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 015280-244100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 129 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-875-811-63

Query Match 96.2%; Score 556; DB 3; Length 129;
Best Local Similarity 96.2%; Pred. No. 3.8e-60;
Matches 100; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ODMLTFQKKHLTNRDVCNNIMSTNLFPHCKDKNTFIYSRPPVKAICKGIASKNVLT 60
DB 26 ODMLTFQKKHLTNRDVCNNIMSTNLFPHCKDKNTFIYSRPPVKAICKGIASKNVLT 85
QY 61 SEFYISDCNVTSRPCKYKLLKSTNFCVTCENQAPVHFVGVGHC 104
DB 86 SEFYISDCNVTSRPCKYKLLKSTNFCVTCENQAPVHFVGVGSC 129

RESULT 5
US-08-875-811-43
Sequence 43, Application US/08875811
Patent No. 6045793
GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Bogue, Luis
APPLICANT: Wlodawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Paris, Susan K.
REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 015280-244100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 379 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-875-811-43
Query Match 96.2%; Score 556; DB 3; Length 379;
Best Local Similarity 96.2%; Pred. No. 1.6e-59;
Matches 100; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 QDWLTFQKHLITNRDVDCNNIMSTNLFHCKDKNTFYISREPVKAICKGIISKVLT 60
Db 26 EDWLTFFQKGIITNRDVDCNNIMSTNLFHCKDKNTFYISREPVKAICKGIISKVLT 85
QY 61 SEFYLSDCVNTSRPCKYKLLKKSNTFCVTCENAPVHFVGHC 104
Db 86 SEFYLSDCVNTSRPCKYKLLKKSNTFCVTCENAPVHFVGSC 129
RESULT 6
US-08-283-971-1
Sequence 1, Application US/08283971
Patent No. 5529775
GENERAL INFORMATION:
APPLICANT: Ardelit Ph.D, Wojciech J.
APPLICANT: Mikulski, Stanislaw M.
TITLE OF INVENTION: PHARMACEUTICAL FOR TREATING TUMORS IN HUMANS
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:

ADDRESSEE: Mark H. Jay, P.C.
STREET: P.O. Box 020083, General Post Office
CITY: Brooklyn
STATE: New York
COUNTRY: USA
ZIP: 11202-0002
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/283,971
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/921,180
FILING DATE: 30-JUL-1992
APPLICATION NUMBER: US 07/178,118
FILING DATE: 06-APR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/436,141
FILING DATE: 13-NOV-1989
ATTORNEY/AGENT INFORMATION:
NAME: Jay, Mark H.
REGISTRATION NUMBER: 27507
REFERENCE/DOCKET NUMBER: 5006 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 718-625-0399
TELEFAX: 718-625-0399
TELEX: No. 5529775 Applicable
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 104 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: N
ANTI-SENSE: N
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Rana pipiens
DEVELOPMENTAL STAGE: Embryo
US-08-283-971-1
Query Match 95.7%; Score 553; DB 1; Length 104;
Best Local Similarity 95.2%; Pred. No. 6.6e-60;
Matches 99; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 1 QDWLTFQKHLITNRDVDCNNIMSTNLFHCKDKNTFYISREPVKAICKGIISKVLT 60
Db 1 EDWLTFFQKGIITNRDVDCNNIMSTNLFHCKDKNTFYISREPVKAICKGIISKVLT 60
QY 61 SEFYLSDCVNTSRPCKYKLLKKSNTFCVTCENAPVHFVGHC 104
Db 61 SEFYLSDCVNTSRPCKYKLLKKSNTFCVTCENAPVHFVGSC 104
RESULT 7
US-07-921-619-1
Sequence 1, Application US/07921619
Patent No. 5595734
GENERAL INFORMATION:
APPLICANT: Ardelit Ph.D, Wojciech J.
APPLICANT: Mikulski, Stanislaw M.
TITLE OF INVENTION: PHARMACEUTICAL FOR TREATING TUMORS IN HUMANS
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mark H. Jay, P.C.
STREET: P.O. Box 020083, General Post Office
CITY: Brooklyn
STATE: New York

COUNTRY: USA
ZIP: 11202-0002
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/921,619
FILING DATE: 19920728
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/178,118
FILING DATE: 06-APR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/436,141
FILING DATE: 13-NOV-1989
ATTORNEY/AGENT INFORMATION:
NAME: Jay, Mark H.
REGISTRATION NUMBER: 27507
REFERENCE/DOCKET NUMBER: 5005 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 718-625-0399
TELEFAX: 718-625-0399
TELEX: No. 5595734 Applicable
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 104 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: N
ANTI-SENSE: N
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Rana pipiens
DEVELOPMENTAL STAGE: Embryo
US-07-921-619-1

Query Match 95.7%; Score 553; DB 1; Length 104;
Best Local Similarity 95.2%; Pred. No. 6,6e-60;
Matches 99; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 1 ODMLFQKHLLNTDVCNNIMSTNLFPHCKDKNTFIYSRPPVPAICKGIIASKNVLT 60
DB 1 EDMLTFQKHLLNTDVCNNIMSTNLFPHCKDKNTFIYSRPPVPAICKGIIASKNVLT 60
QY 61 SEFYISDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 104
DB 61 SEFYISDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGSC 104

RESULT 8
US-08-467-955-1
Sequence 1, Application US/08467955
Patent No. 5728805
GENERAL INFORMATION:
APPLICANT: Aidelit Ph.D. Wojciech J.
TITLE OF INVENTION: PHARMACEUTICALS AND METHOD FOR MAKING THEM
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mark H. Jay, P.A.
STREET: P.O. Box E
CITY: Short Hills
STATE: New Jersey
COUNTRY: USA
ZIP: 07078-0383
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,955
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/178,118
FILING DATE: 06-APR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/436,141
FILING DATE: 13-NOV-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/814,332
FILING DATE: 03-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/283,970
FILING DATE: 01-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Jay, Mark H.
REGISTRATION NUMBER: 27507
REFERENCE/DOCKET NUMBER: 5007 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-912-9066
TELEFAX: 201-912-0442
TELEX: No. 5728805 Applicable
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 104 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: N
ANTI-SENSE: N
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Rana pipiens
DEVELOPMENTAL STAGE: Oocyte
US-08-467-955-1

Query Match 95.7%; Score 553; DB 1; Length 104;
Best Local Similarity 95.2%; Pred. No. 6,6e-60;
Matches 99; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 1 ODMLFQKHLLNTDVCNNIMSTNLFPHCKDKNTFIYSRPPVPAICKGIIASKNVLT 60
DB 1 EDMLTFQKHLLNTDVCNNIMSTNLFPHCKDKNTFIYSRPPVPAICKGIIASKNVLT 60
QY 61 SEFYISDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 104
DB 61 SEFYISDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGSC 104

RESULT 9
US-08-891-848-13
Sequence 13, Application US/08891848
Patent No. 5955073
GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Youle, Richard J.
APPLICANT: Newton, Dianne L.
APPLICANT: Nicholas, Peter J.
TITLE OF INVENTION: Selective Rhase Cytotoxic Reagents
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

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? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patentin Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/891,848
? FILING DATE: No. 5955073 yet assigned
? CLASSIFICATION: 530
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 08/125,462
? FILING DATE: 22-SEP-1993
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 08/014,082
? FILING DATE: 04-FEB-1993
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 07/779,195
? FILING DATE: 22-OCT-1991
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 07/510,696
? FILING DATE: 20-APR-1990
? ATTORNEY/AGENT INFORMATION:
? NAME: Weber, Ellen Lauver
? REGISTRATION NUMBER: 32,762
? REFERENCE/DOCKET NUMBER: 015280-110310US
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (415) 576-0200
? TELEFAX: (415) 576-0300
? INFORMATION FOR SEQ ID NO: 13:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 104 amino acids
? TYPE: amino acid
? STRANDEDNESS:
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? FEATURE:
? NAME/KEY: Protein
? LOCATION: 1..104
? OTHER INFORMATION: /label= Onc
? US-08-891-848-13
? note= "Oncogene from Rana pipiens"

Query Match 95.7%; Score 553; DB 2; Length 104;
Best Local Similarity 95.2%; Pred. No. 6.6e-60;
Matches 99; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QDWLTFQKKHLTNTDQVDCNNIMSTNLFPHCKDKNTFIYSRPPVPAICGIIASKNVLT 60
Db 1 EDWLTFQKKHLTNTDQVDCNNIMSTNLFPHCKDKNTFIYSRPPVPAICGIIASKNVLT 60
Qy 61 SEFYISDCNVTSRPCKYKLYKSTNTFCVTCENQAPVHFVGVGHC 104
Db 61 SEFYISDCNVTSRPCKYKLYKSTNTFCVTCENQAPVHFVGVGSC 104

RESULT 10
US-08-875-811-39
? Sequence 39, Application US/08875811
? Patent No. 6045793
? GENERAL INFORMATION:
? APPLICANT: Rybak, Susanna M.
? APPLICANT: Newton, Dianne L.
? APPLICANT: Boque, Luis
? APPLICANT: Wlodawer, Alexander
? TITLE OF INVENTION: Recombinant Ribonuclease Proteins
? NUMBER OF SEQUENCES: 64
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Townsend and Townsend and Crew LLP
? STREET: Two Embarcadero Center, Eighth Floor
? CITY: San Francisco
? STATE: California
? COUNTRY: USA
? ZIP: 94111-3834
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? FILING DATE: 21-FEB-1996
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? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patentin Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/875,811
? FILING DATE: 19-FEB-1998
? CLASSIFICATION: 435
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: NO PCT/US97/02588
? FILING DATE: 19-FEB-1997
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 60/011,800
? FILING DATE: 21-FEB-1996
? ATTORNEY/AGENT INFORMATION:
? NAME: Faris, Susan K.
? REGISTRATION NUMBER: 41,739
? REFERENCE/DOCKET NUMBER: 015280-244100US
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (415) 576-0200
? TELEFAX: (415) 576-0300
? INFORMATION FOR SEQ ID NO: 39:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 105 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? US-08-875-811-39

Query Match 95.7%; Score 553; DB 3; Length 105;
Best Local Similarity 95.2%; Pred. No. 6.7e-60;
Matches 99; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QDWLTFQKKHLTNTDQVDCNNIMSTNLFPHCKDKNTFIYSRPPVPAICGIIASKNVLT 60
Db 2 EDWLTFQKKHLTNTDQVDCNNIMSTNLFPHCKDKNTFIYSRPPVPAICGIIASKNVLT 61
Qy 61 SEFYISDCNVTSRPCKYKLYKSTNTFCVTCENQAPVHFVGVGHC 104
Db 62 SEFYISDCNVTSRPCKYKLYKSTNTFCVTCENQAPVHFVGVGSC 105

RESULT 11
US-08-875-811-41
? Sequence 41, Application US/08875811
? Patent No. 6045793
? GENERAL INFORMATION:
? APPLICANT: Rybak, Susanna M.
? APPLICANT: Newton, Dianne L.
? APPLICANT: Boque, Luis
? APPLICANT: Wlodawer, Alexander
? TITLE OF INVENTION: Recombinant Ribonuclease Proteins
? NUMBER OF SEQUENCES: 64
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Townsend and Townsend and Crew LLP
? STREET: Two Embarcadero Center, Eighth Floor
? CITY: San Francisco
? STATE: California
? COUNTRY: USA
? ZIP: 94111-3834
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patentin Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/875,811
? FILING DATE: 19-FEB-1998
? CLASSIFICATION: 435
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: NO PCT/US97/02588
? FILING DATE: 19-FEB-1997
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 60/011,800
? FILING DATE: 21-FEB-1996
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ATTORNEY/AGENT INFORMATION:
NAME: Farris, Susan K.
REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 015280-244100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-875-811-41

Query Match 95.7%; Score 553; DB 3; Length 355;
Best Local Similarity 95.2%; Pred. No. 3,3e-59;
Matches 99; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 QDWLTQKQKHLNTRVDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAIKGIISKVLT 60
DB 252 EDWLTQKQKHLNTRVDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAIKGIISKVLT 311
QY 61 SEFYLSDCNVTSPCKYKLLKSTNFCVTCENQAPVHFGVGC 104
DB 312 SEFYLSDCNVTSPCKYKLLKSTNFCVTCENQAPVHFGVGC 355

RESULT 12
US-08-875-811-51
Sequence 51, Application US/08875811
Patent No. 6045793
GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Bogue, Luis
APPLICANT: Mlodawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Farris, Susan K.
REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 015280-244100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 358 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-875-811-51

Query Match 95.7%; Score 553; DB 3; Length 358;
Best Local Similarity 95.2%; Pred. No. 3,4e-59;
Matches 99; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 QDWLTQKQKHLNTRVDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAIKGIISKVLT 60
DB 2 EDWLTQKQKHLNTRVDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAIKGIISKVLT 61
QY 61 SEFYLSDCNVTSPCKYKLLKSTNFCVTCENQAPVHFGVGC 104
DB 62 SEFYLSDCNVTSPCKYKLLKSTNFCVTCENQAPVHFGVGC 105

RESULT 13
US-08-875-811-1
Sequence 1, Application US/08875811
Patent No. 6045793
GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Bogue, Luis
APPLICANT: Mlodawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Farris, Susan K.
REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 015280-244100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 104 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..104
OTHER INFORMATION: /label=nonc
OTHER INFORMATION: /note="native ONCOMASE (registered
OTHER INFORMATION: Trademark) from Rana pipiens"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: /note="Xaa = pyroglutamic acid"

US-08-875-811-1

Query Match 95.3%; Score 551; DB 3; Length 104;
Best Local Similarity 96.1%; Pred. No. 1.2e-59;
Matches 99; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 DMLTFQKHILTNTRVDNCCNINIMSTNLFHCKDKNTFTYSRPEPVKAICKGIASKNVLTTS 61
DB 2 DMLTFQKHILTNTRVDNCCNINIMSTNLFHCKDKNTFTYSRPEPVKAICKGIASKNVLTTS 61
QY 62 EFLYSDCNVTSRPPCKYKLLKSKSTNTFCVTCENQAPVHPFVGSHC 104
DB 62 EFLYSDCNVTSRPPCKYKLLKSKSTNTFCVTCENQAPVHPFVGSHC 104

RESULT 14

US-09-071-672-1
Sequence 1, Application US/09071672
Patent No. 6393276
GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Goldenberg, David M.
TITLE OF INVENTION: Immunotoxins Directed Against Malignant
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071.672
FILING DATE: 01-MAY-1998
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/046.895
FILING DATE: 02-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 015280-32510US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 104 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: /product= "OTHER"
OTHER INFORMATION: /note= "Xaa = Glu or pyroglutamic acid"
FEATURE:
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LOCATION: 1..104
OTHER INFORMATION: /note= "RNase A derived from
OTHER INFORMATION: Rana pipiens, "onc protein"
US-09-071-672-1

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Best Local Similarity 96.1%; Pred. No. 1.2e-59;

Matches 99; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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DB 2 DMLTFQKHILTNTRVDNCCNINIMSTNLFHCKDKNTFTYSRPEPVKAICKGIASKNVLTTS 61
QY 62 EFLYSDCNVTSRPPCKYKLLKSKSTNTFCVTCENQAPVHPFVGSHC 104
DB 62 EFLYSDCNVTSRPPCKYKLLKSKSTNTFCVTCENQAPVHPFVGSHC 104

RESULT 15

US-08-875-811-28
Sequence 28, Application US/08875811
Patent No. 6045793
GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Boque, Luis
APPLICANT: Wlodawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875.811
FILING DATE: 19-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011.800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Paris, Susan K.
REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 015280-244100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 106 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-875-811-28

Query Match 95.3%; Score 551; DB 3; Length 106;
Best Local Similarity 96.1%; Pred. No. 1.2e-59;
Matches 99; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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DB 64 EFLYSDCNVTSRPPCKYKLLKSKSTNTFCVTCENQAPVHPFVGSHC 106

Search completed: January 22, 2004, 12:10:05

Job time : 12.4644 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 22, 2004, 12:01:20 (Search time 32.7191 Seconds
(without alignment)
504.524 Million cell updates/sec

Title: US-09-622-613C-4
Perfect score: 577
Sequence: 1 QDWLTFQKXHLNTRDVDCN.....TFCVTCENQAPVHFVGVGHC 104

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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7	570	98.8	105	20	AA28871
8	555	96.2	104	18	AA06544
9	553	95.8	104	18	AA03031

10	553	95.8	104	22	AA031666
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12	553	95.8	379	18	AA035126
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21	550	95.3	104	22	AA031667
22	550	95.3	104	23	AB031617
23	550	95.3	105	18	AA035123
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25	550	95.3	355	18	AA035125
26	550	95.3	358	18	AA035130
27	548	95.0	106	18	AA035122
28	548	95.0	107	18	AA035117
29	548	95.0	112	18	AA035118
30	548	95.0	251	18	AA035134
31	548	95.0	254	18	AA035135
32	548	95.0	355	18	AA035129
33	548	95.0	355	18	AA035133
34	548	95.0	366	18	AA035132
35	545	94.5	104	18	AA018224
36	543	94.1	105	18	AA035115
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45	286	49.6	111	20	AA033321

ALIGNMENTS

RESULT 1
ID AAY28866
AAY28866 standard; Protein; 104 AA.

XX AAY28866;
XX 25-JAN-2000 (first entry)

DT Recombinant RapLRI Met23Leu amino acid sequence.

DE Recombinant Rana pipiens ribonuclease; RapLRI Met23Leu; covalently bound;
XX LL2 antibody; ligand binding moiety; CD22; cancerous B cell; RNase;
KW Kaposi's sarcoma; human chorionic gonadotropin; hCG; signal peptide;
KW recombinant ribonuclease; cytotoxic fusion protein; cancer; frog;
KW autoimmune disease.

KW Rana pipiens.
XX Synthetic.

OS Rana pipiens.
OS Synthetic.
FH Key Location/Qualifiers
FT MISC-difference 23 /note= "Wild type Met replaced with Leu"
FT PT

FN W09950398-A2.

XX 07-OCT-1999.

PD 26-MAR-1999; 99WO-US06641.

XX 27-MAR-1998; 98US-0079751.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

```

XX  Newton DL, Rybak SM;
PI
XX
DR  MPI: 1999-610847/52.
DR  N-PSDB; AA208125.
XX
PT  New recombinant ribonucleases, used for killing target cells, e.g. for
PT  treating cancers, viral infections or autoimmune diseases -
XX
PS  Claim 34; Page 56; 71pp; English.
XX
CC  The present sequence is a recombinant Rana pipiens ribonuclease (RapLRI)
CC  protein with Met23Leu. Carboxy terminal end of recombinant RapLRI has a
CC  covalently bound ligand binding moiety, which can be a Ll2 antibody
CC  directed against CD22 on cancerous B cells or human chorionic
CC  gonadotropin (hCG) effective against Kaposi's sarcoma cells. Recombinant
CC  ribonucleases can be expressed in bacteria without an N-terminal
CC  methionine due to the presence of a signal peptide that is cleaved by
CC  bacteria. The soluble expression of ribonuclease allows the proteins to
CC  be fused in-frame with ligand binding moieties to form cytotoxic fusion
CC  proteins. They can be used for treatment of cancer and autoimmune
CC  diseases.
XX
SQ  Sequence 104 AA:

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Best Local Similarity 100.0%; Pred. No. 4.5e-62;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 QDMLTFQKGLTNTRDVDCNNILSTNLFPHCKDKNTFIYSRPPVKAICKGIASKVLT 60
OY 61 SEFYLSDCNVTSRPCRYKLKSTNTFCVTCENQAPVHFVGCHC 104
DB 61 SEFYLSDCNVTSRPCRYKLKSTNTFCVTCENQAPVHFVGCHC 104

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ID  AAY28869 standard; Protein; 105 AA.
AC  AAY28869;
XX
DT  25-JAN-2000 (first entry)
XX
DE  Recombinant Met(-1) RapLRI Met23Leu-(His)6 protein.
XX
KM  Recombinant Met(-1) Rana pipiens ribonuclease Met23Leu-(His)6; RapLRI;
KM  CD22; covalently bound; Ll2 antibody; ligand binding moiety; RNase;
KM  cancerous B cell; Kaposi's sarcoma; human chorionic gonadotropin; hCG;
KM  signal peptide; recombinant ribonuclease; cytotoxic fusion protein;
KM  cancer; frog; autoimmune disease.
XX
XX  Rana pipiens.
OS  Synthetic.
OS
FH  Key Location/Qualifiers
FT  Misc-difference 1 /note= "(His)6 histidine tag attached to N-terminal Met"
FT  Misc-difference 1 /note= "Met not found in wild type RapLRI"
FT  Misc-difference 24 /note= "Wild type Met replaced with Leu"
FT
XX  WO950398-A2.
XX  07-OCT-1999.
XX  26-MAR-1999; 99WO-US06641.
XX  27-MAR-1998; 98US-0079751.
XX

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PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX  Newton DL, Rybak SM;
XX
DR  MPI: 1999-610847/52.
DR  N-PSDB; AA208127.
XX
PT  New recombinant ribonucleases, used for killing target cells, e.g. for
PT  treating cancers, viral infections or autoimmune diseases -
XX
PS  Claim 4; Page 59; 71pp; English.
XX
CC  The present sequence is a recombinant Rana pipiens ribonuclease protein
CC  (RapLRI) with Met at position 1 attached to (His)6 tag and Met24Leu.
CC  Carboxy terminal end of recombinant RapLRI has a covalently bound ligand
CC  binding moiety, which can be a Ll2 antibody directed against CD22 on
CC  cancerous B cells or human chorionic gonadotropin (hCG) effective
CC  against Kaposi's sarcoma cells. Recombinant ribonucleases can be
CC  expressed in bacteria without an N-terminal methionine due to the
CC  presence of a signal peptide that is cleaved by bacteria. The soluble
CC  expression of ribonuclease allows the proteins to be fused in-frame with
CC  ligand binding moieties to form cytotoxic fusion proteins. They can be
CC  used for treatment of cancer and autoimmune diseases.
XX
SQ  Sequence 105 AA:

Query Match 100.0%; Score 577; DB 20; Length 105;
Best Local Similarity 100.0%; Pred. No. 4.6e-62;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 2 QDMLTFQKGLTNTRDVDCNNILSTNLFPHCKDKNTFIYSRPPVKAICKGIASKVLT 61
OY 61 SEFYLSDCNVTSRPCRYKLKSTNTFCVTCENQAPVHFVGCHC 104
DB 62 SEFYLSDCNVTSRPCRYKLKSTNTFCVTCENQAPVHFVGCHC 105

RESULT 3
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ID  AAY28865 standard; Protein; 104 AA.
AC  AAY28865;
XX
DT  25-JAN-2000 (first entry)
XX
DE  Rana pipiens liver ribonuclease (RapLRI).
XX
KM  Rana pipiens liver ribonuclease; RapLRI; covalently bound; Ll2 antibody;
KM  ligand binding moiety; CD22; cancerous B cell; Kaposi's Sarcoma; frog;
KM  human chorionic gonadotropin; hCG; recombinant ribonuclease; RNase;
KM  signal peptide; cytotoxic fusion protein; cancer; autoimmune disease.
XX
XX  Rana pipiens.
OS
OS  WO950398-A2.
XX  07-OCT-1999.
XX  26-MAR-1999; 99WO-US06641.
XX  27-MAR-1998; 98US-0079751.
XX
XX  (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX  Newton DL, Rybak SM;
XX
DR  MPI: 1999-610847/52.
DR  N-PSDB; AA208124.
XX
PT  New recombinant ribonucleases, used for killing target cells, e.g. for
PT  treating cancers, viral infections or autoimmune diseases -
XX

```

XX Claim 1; Page 55; 71pp; English.

XX The present sequence is Rana pipiens liver ribonuclease (RapLr1)

CC protein. Carboxy terminal end of RapLr1 has a covalently bound

CC ligand binding moiety, which can be a Lf2 antibody directed against

CC CD22 on cancerous B cells or human chorionic gonadotrophin (hCG)

CC effective against Kaposi's Sarcoma cells. Recombinant ribonucleases can

CC be expressed in bacteria without an N-terminal methionine due to the

CC presence of a signal peptide that is cleaved by bacteria. The soluble

CC expression of ribonuclease allows the proteins to be fused in-frame with

CC ligand binding moieties to form cytotoxic fusion proteins. They can be

CC used for treatment of cancer and autoimmune diseases.

XX

SQ Sequence 104 AA;

Query Match 99.7%; Score 575; DB 20; Length 104;

Beat Local Similarity 99.0%; Pred. No. 7,9e-62;

Matches 103; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QDWLTFQKXHLTNTRDVCNNILSTNLFPHCKDKNTFIYSRPEPVKAICKGIIASGNVLT 60

DB 1 QDWLTFQKXHLTNTRDVCNNIMSTNLFPHCKDKNTFIYSRPEPVKAICKGIIASGNVLT 60

QY 61 SEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGCHC 104

DB 61 SEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGCHC 104

RESULT 4

AAy28867 ID AAY28867 standard; Protein; 105 AA.

XX AAY28867;

XX 25-JAN-2000 (first entry)

DT Recombinant Met(-1) RapLr1.

XX

XX Recombinant Met(-1) Rana pipiens ribonuclease; RapLr1; CD22; RNase;

XX covalently bound; Lf2 antibody; ligand binding moiety; cancerous B cell;

KM Kaposi's sarcoma; human chorionic gonadotrophin; hCG; signal peptide;

KM recombinant ribonuclease; cytotoxic fusion protein; cancer; frog;

KM autoimmune disease.

XX

XX Rana pipiens.

OS Synthetic.

OS

XX

XX Key Location/Qualifiers

FT Misc-difference 1 /note= "Met not found in wild type RapLr1"

FT

XX

XX W09950398-A2.

XX

XX 07-OCT-1999.

XX

XX 26-MAR-1999; 99WO-US06641.

XX

XX 27-MAR-1998; 98US-0079751.

XX

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

PA

XX

PI Newton DL, Rybak SM;

XX

XX WPI; 1999-610847/52.

DR

XX

XX N-PSDB; AA208126.

XX

XX New recombinant ribonucleases, used for killing target cells, e.g. for

PT treating cancers, viral infections or autoimmune diseases -

XX

XX Claim 34; Page 57; 71pp; English.

XX

XX The present sequence is a recombinant Rana pipiens ribonuclease (RapLr1)

CC

CC protein with Met at position 1. Carboxy terminal end of recombinant

CC RapLr1 has a covalently bound ligand binding moiety, which can be a Lf2

CC antibody directed against CD22 on cancerous B cells or human chorionic

CC gonadotrophin (hCG) effective against Kaposi's sarcoma cells. Recombinant

CC ribonucleases can be expressed in bacteria without an N-terminal

CC methionine due to the presence of a signal peptide that is cleaved by

CC bacteria. The soluble expression of ribonuclease allows the proteins to

CC be fused in-frame with ligand binding moieties to form cytotoxic fusion

CC proteins. They can be used for treatment of cancer and autoimmune

CC diseases.

XX

SQ Sequence 105 AA;

Query Match 99.7%; Score 575; DB 20; Length 105;

Beat Local Similarity 99.0%; Pred. No. 8e-62;

Matches 103; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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DB 2 QDWLTFQKXHLTNTRDVCNNIMSTNLFPHCKDKNTFIYSRPEPVKAICKGIIASGNVLT 61

QY 61 SEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGCHC 104

DB 62 SEFYLSDCNVTSRPCKYKLKKSTNTFCVTCENQAPVHFVGCHC 105

RESULT 5

AAy28879 ID AAY28879 standard; Protein; 127 AA.

XX AAY28879;

XX 25-JAN-2000 (first entry)

DT Rana pipiens Clone 5a1b ribonuclease.

XX

XX Rana pipiens ribonuclease Clone 5a1b; RapLr1; covalently bound; RNase;

XX Lf2 antibody; ligand binding moiety; CD22; cancerous B cell; oncogene;

KM Kaposi's Sarcoma; human chorionic gonadotrophin; hCG; cancer;

KM recombinant ribonuclease; frog; signal peptide; cytotoxic fusion protein;

KM autoimmune disease.

XX

XX Rana pipiens.

OS

OS

XX

XX Key Location/Qualifiers

FT Peptide 1..23

FT /label= "Signal peptide"

FT /note= "Putative"

FT Protein 24..127

FT /label= Rana_pipiens_Clone_5a1b_ribonuclease

FT

XX

XX W09950398-A2.

XX

XX 07-OCT-1999.

XX

XX 26-MAR-1999; 99WO-US06641.

XX

XX 27-MAR-1998; 98US-0079751.

XX

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

PA

XX

PI Newton DL, Rybak SM;

XX

XX WPI; 1999-610847/52.

DR

XX

XX N-PSDB; AA208136.

XX

XX New recombinant ribonucleases, used for killing target cells, e.g. for

PT treating cancers, viral infections or autoimmune diseases -

XX

XX Disclosure; Page 69; 71pp; English.

XX

XX The present sequence is a Rana pipiens Clone 5a1b ribonuclease (RapLr1).

CC It is encoded by Clone 5a1b cDNA obtained from Rana pipiens liver mRNA

CC

CC library. It exhibits differences with Oncotase (RTM) at amino acid
CC residues 11, 20, 85 and 103. Carboxy terminal end of RapLRI has a
CC covalently bound ligand binding moiety, which can be a LL2 antibody
CC directed against CD22 on cancerous B cells or human chorionic
CC gonadotrophin (hCG) effective against Kaposi's Sarcoma cells. Recombinant
CC ribonucleases can be expressed in bacteria without an N-terminal
CC methionine due to the presence of a signal peptide that is cleaved by
CC bacteria. The soluble expression of ribonuclease allows the proteins to
CC be fused in-frame with ligand binding moieties to form cytotoxic fusion
CC proteins. They can be used for treatment of cancer and autoimmune
CC diseases.

XX SQ Sequence 127 AA;
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XX Query Match 99.7%; Score 575; DB 20; Length 127;
XX Best Local Similarity 99.0%; Pred. No. 1e-61;
XX Matches 103; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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DB 24 QDMLTFQKHLLNTNTRDVCNNIMSTNLFHCKDKNTFIYSRPPVKAICKGIASKVLT 83
OY 61 SEFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGHC 104
DB 84 SEFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGHC 127

RESULT 6
AAZ28870
ID AAZ28870 standard; Protein; 104 AA.
XX
XX AAZ28870;
XX
XX 25-JAN-2000 (first entry)
XX
XX Recombinant RapLRI GlnSer amino acid sequence.
XX
XX Recombinant Rana pipiens ribonuclease; RapLRI GlnSer; covalently bound;
XX LL2 antibody; ligand binding moiety; CD22; cancerous B cell; frog;
XX Kaposi's sarcoma; human chorionic gonadotrophin; hCG; signal peptide;
XX recombinant ribonuclease; cytotoxic fusion protein; cancer; RNase;
XX autoimmune disease.
XX
XX Rana pipiens.
XX Synthetic.
XX
XX Key Location/Qualifiers
XX FT Misc-difference 1 /note= "Wild type Gln replaced with Ser"
XX FT
XX FT
XX PN WO9950398-A2.
XX
XX PD 07-OCT-1999.
XX
XX PF 26-MAR-1999; 99WO-US06641.
XX
XX PR 27-MAR-1998; 98US-0079751.
XX
XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
XX PI Newton DL, Rybak SM;
XX
XX WP1; 1999-610847/52.
XX DR N-PSDB; AA208128.
XX
XX PT New recombinant ribonucleases, used for killing target cells, e.g. for
XX treating cancers, viral infections or autoimmune diseases -
XX
XX PS Claim 34; Page 60; 71pp; English.
XX
XX The present sequence is a recombinant Rana pipiens ribonuclease (RapLRI)
XX protein with GlnSer. Carboxy terminal end of recombinant RapLRI has a
XX covalently bound ligand binding moiety, which can be a LL2 antibody

CC directed against CD22 on cancerous B cells or human chorionic
CC gonadotrophin (hCG) effective against Kaposi's sarcoma cells. Recombinant
CC ribonucleases can be expressed in bacteria without an N-terminal
CC methionine due to the presence of a signal peptide that is cleaved by
CC bacteria. The soluble expression of ribonuclease allows the proteins to
CC be fused in-frame with ligand binding moieties to form cytotoxic fusion
CC proteins. They can be used for treatment of cancer and autoimmune
CC diseases.

XX SQ Sequence 104 AA;
XX
XX Query Match 98.8%; Score 570; DB 20; Length 104;
XX Best Local Similarity 99.0%; Pred. No. 3.2e-61;
XX Matches 102; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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OY 62 EFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGHC 104
DB 62 EFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGHC 104

RESULT 7
AAZ28871
ID AAZ28871 standard; Protein; 105 AA.
XX
XX AAZ28871;
XX
XX 25-JAN-2000 (first entry)
XX
XX Recombinant Met(-1) RapLRI GlnSer amino acid sequence.
XX
XX Recombinant Met(-1) Rana pipiens ribonuclease GlnSer; RapLRI; CD22;
XX covalently bound; LL2 antibody; ligand binding moiety; cancerous B cell;
XX Kaposi's sarcoma; human chorionic gonadotrophin; hCG; signal peptide;
XX recombinant ribonuclease; cytotoxic fusion protein; cancer; frog;
XX autoimmune disease; RNase.
XX
XX Rana pipiens.
XX Synthetic.
XX
XX Key Location/Qualifiers
XX FT Misc-difference 1 /note= "Met not found in wild type RapLRI"
XX FT
XX FT
XX FT Misc-difference 2 /note= "Wild type Gln replaced with Ser"
XX FT
XX PN WO9950398-A2.
XX
XX PD 07-OCT-1999.
XX
XX PF 26-MAR-1999; 99WO-US06641.
XX
XX PR 27-MAR-1998; 98US-0079751.
XX
XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
XX PI Newton DL, Rybak SM;
XX
XX WP1; 1999-610847/52.
XX DR N-PSDB; AA208129.
XX
XX PT New recombinant ribonucleases, used for killing target cells, e.g. for
XX treating cancers, viral infections or autoimmune diseases -
XX
XX PS Claim 34; Page 61; 71pp; English.
XX
XX The present sequence is a recombinant Rana pipiens ribonuclease (RapLRI)
XX protein with Met at position 1 and GlnSer. Carboxy terminal end of
XX recombinant RapLRI has a covalently bound ligand binding moiety, which
XX can be a LL2 antibody directed against CD22 on cancerous B cells or human

DE Amino acid sequence of a frog ribonuclease protein.
 XX
 KW Frog; ribonuclease; ranpirinase; RNase.
 XX
 OS Rana pipiens.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 1 /note= "this Gln is autocyclised to pyroglutamic acid"
 FT
 XX US6175003-B1.
 PN 16-JAN-2001.
 PD
 XX 10-SEP-1999; 99US-0394268.
 PF
 XX 10-SEP-1999; 99US-0394268.
 PR 10-SEP-1999; 99US-0394268.
 XX
 PA (ALFA-) ALFACELL CORP.
 XX
 PI Saxena SK;
 XX
 DR WPI; 2001-167808/17.
 XX
 PT New nucleic acids encoding a ribonuclease (Rnase), useful for the
 PT precise targeting of Rnase to a predetermined cell receptor -
 XX
 PS Claim 1; Columns 5-6; 7pp; English.
 XX
 CC The present sequence represents a frog ribonuclease protein (ranpirinase)
 CC (Rnase). The specification describes a synthetic ribonuclease protein,
 CC in which the addition of cysteine in the ribonuclease facilitates the
 CC chemical linking of a targeting molecule by the single reactive
 CC sulfhydryl group. The specification also describes a method for the
 CC production of ranpirinase using DNA technology instead of processing
 CC biological material. The re-engineering of the protein molecule allows
 CC easier attachment to a targeting molecule thereby making it possible for
 CC the ribonuclease to be delivered to a particular cell receptor where it
 CC might be most effective.
 CC
 SQ Sequence 104 AA;
 XX
 XX
 Query Match 95.8%; Score 553; DB 22; Length 104;
 Best Local Similarity 95.2%; Pred. No. 3.7e-59;
 Matches 99; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 QY 1 QDMLTFQKXHLTNRDVCNNILSTNLFHCKDKNTFIYSRBPVKAICKGIIASKNVLT 60
 DB 1 QDMLTFQKXHLTNRDVCNNILSTNLFHCKDKNTFIYSRBPVKAICKGIIASKNVLT 60
 QY 61 SEFYISDCNVTSRPCKYKLLKSTNTFCYTCENQAPVHFVGVGHC 104
 DB 61 SEFYISDCNVTSRPCKYKLLKSTNTFCYTCENQAPVHFVGVGSC 104
 XX
 RESULT 11
 ABG32650
 ID ABG32650 standard; Protein; 104 AA.
 XX
 AC ABG32650;
 XX
 DT 15-NOV-2002 (first entry)
 XX
 DE Northern leopard frog ranpirinase protein.
 XX
 KW Northern leopard frog; ranpirinase; site-directed mutation; ribonuclease.
 XX
 OS Rana pipiens.
 XX
 PN US6423515-B1.
 XX
 PD 23-JUL-2002.

PF 14-OCT-2000; 2000US-0687748.
 XX
 PR 10-SEP-1999; 99US-0394268.
 XX
 PA (ALFA-) ALFACELL CORP.
 XX
 PI Saxena SK;
 XX
 DR WPI; 2002-664633/71.
 XX
 PT Constructing isolated nucleic acid encoding ribonuclease, by subjecting
 PT desired recombinant plasmid DNA to different site-directed mutations to
 PT produce nucleic acid, using different polymerase chain reaction
 PT protocols -
 XX
 PS Claim 1; Column 5-6; 8pp; English.
 XX
 CC The present invention relates to a new method of constructing isolated
 CC nucleic acid encoding ribonuclease protein with N-terminal Met at
 CC position -1 and Glu at position 1, where its Met has been cleaved and
 CC its Glu has been autocyclised. The method of the invention involves
 CC subjecting pERR1d-rOnc(Q1,M23L) plasmid DNA to two different
 CC site-directed mutations, each using overlapping PCR protocol. The method
 CC is useful for constructing an isolated nucleic acid encoding the
 CC ribonuclease. The present amino acid sequence represents the northern
 CC leopard frog ranpirinase protein of the invention.
 CC
 SQ Sequence 104 AA;
 XX
 XX
 Query Match 95.8%; Score 553; DB 23; Length 104;
 Best Local Similarity 95.2%; Pred. No. 3.7e-59;
 Matches 99; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 QY 1 QDMLTFQKXHLTNRDVCNNILSTNLFHCKDKNTFIYSRBPVKAICKGIIASKNVLT 60
 DB 1 QDMLTFQKXHLTNRDVCNNILSTNLFHCKDKNTFIYSRBPVKAICKGIIASKNVLT 60
 QY 61 SEFYISDCNVTSRPCKYKLLKSTNTFCYTCENQAPVHFVGVGHC 104
 DB 61 SEFYISDCNVTSRPCKYKLLKSTNTFCYTCENQAPVHFVGVGSC 104
 XX
 RESULT 12
 AAM35126
 ID AAM35126 standard; Protein; 379 AA.
 XX
 AC AAM35126;
 XX
 DT 20-APR-1998 (first entry)
 XX
 DE R. pipiens recombinant RNase rOnc fusion protein 2.
 XX
 KW RNase A; ribonuclease; cytotoxic; onconase; nOnc; immunofusion;
 KW tumour cell growth; frog.
 XX
 OS Rana pipiens.
 XX
 OS Synthetic.
 XX
 PN WO9731116-A2.
 XX
 PD 28-AUG-1997.
 XX
 PF 19-FEB-1997; 97WO-US02588.
 XX
 PR 21-FEB-1996; 96US-0011800.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Boque L, Newton DL, Rybak SM, Wlodawer A;
 XX
 DR WPI; 1997-435168/40.
 DR N-PSDB; AAT94964.
 XX

CC cinoma HT-520 cells.

XX Sequence 104 AA;

Query Match 95.3%; Score 550; DB 12; Length 104;
Best Local Similarity 94.2%; Pred. No. 8.5e-59;
Matches 98; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 1 ODMLTFOKKHLTNTBDVDCNNILSTNLFPHCKDKNTFIYSRPEPVKAICKGIASKNVLT 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 1 EDMLTFOKKHLTNTBDVDCNNILSTNLFPHCKDKNTFIYSRPEPVKAICKGIASKNVLT 60

OY 61 SEFYISDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 104
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 61 SEFYISDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGSC 104

RESULT 15

AAR47303
ID AAR47303 standard, protein, 104 AA.

XX AAR47303;

XX 25-MAR-2003 (updated)
DT 09-SEP-1994 (first entry)

XX ONCONASE (pharmaceutical protein).

XX Onconase; pharmaceutical; protein; adenocarcinoma; treatment;
KM cisplatin; melphalan; adriamycin; ovarian cancer; ovary.

XX Synthetic.

XX WO9403197-A1.

XX 17-FEB-1994.

XX 02-JUL-1993; 93WO-US06357.

XX PR 30-JUL-1992; 92US-0921180.

XX (ALFA-) ALFACELL CORP.

XX Ardelt WJ, Mikuleki SM;

XX WPI; 1994-063396/08.

XX Pharmaceutical contg. Cisplatin, Melphalan or Adriamycin - active
PT in-vitro against OVCAR-3 human ovarian adenocarcinoma cells

XX Claim 7; Page 13; 18pp; English.

XX This pharmaceutical protein (ONCONASE) is used in the production of
CC a bioactive pharmaceutical composition also comprising one of
CC Cisplatin (cis-diamminedichloroplatinum), Melphalan, (4-[bis-(2-
CC chloroethyl)amino]-L-phenylamine) or Adriamycin (doxorubicin HCl).
CC The composition has bioactivity in vitro against OVCAR-3 human
CC ovarian adenocarcinoma cells.
CC (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 104 AA;

Query Match 95.3%; Score 550; DB 15; Length 104;
Best Local Similarity 94.2%; Pred. No. 8.5e-59;
Matches 98; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 1 ODMLTFOKKHLTNTBDVDCNNILSTNLFPHCKDKNTFIYSRPEPVKAICKGIASKNVLT 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 1 EDMLTFOKKHLTNTBDVDCNNILSTNLFPHCKDKNTFIYSRPEPVKAICKGIASKNVLT 60

OY 61 SEFYISDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 104
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 61 SEFYISDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGSC 104

Search completed: January 22, 2004, 12:06:23
Job time : 33.7191 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model1

Run on: January 22, 2004, 12:01:30 (Search time 12.4644 Seconds
(without alignments)
353.031 Million cell updates/sec

Title: US-09-622-613C-4

Perfect score: 577
1 QDMLTFQKKHLTNTRDVDCN.....TFCVTCENQAPVHFVGVGHC 104

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep.*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/PTCUS.COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	555	96.2	104	1	US-08-467-955-2
2	553	95.8	104	3	US-09-394-268-1
3	553	95.8	104	4	US-09-687-748-1
4	553	95.8	129	3	US-08-875-811-63
5	553	95.8	379	3	US-08-875-811-43
6	550	95.3	104	1	US-08-283-971-1
7	550	95.3	104	1	US-07-921-619-1
8	550	95.3	104	1	US-08-467-955-1
9	550	95.3	104	2	US-08-891-848-13
10	550	95.3	104	4	US-09-394-268-2
11	550	95.3	104	3	US-09-687-748-2
12	550	95.3	105	3	US-08-875-811-39
13	550	95.3	355	3	US-08-875-811-41
14	550	95.3	358	3	US-08-875-811-51
15	548	95.0	104	4	US-08-875-811-1
16	548	95.0	104	3	US-09-071-672-1
17	548	95.0	106	3	US-08-875-811-28
18	548	95.0	107	3	US-08-875-811-30
19	548	95.0	112	3	US-08-875-811-32
20	548	95.0	251	3	US-08-875-811-59
21	548	95.0	254	3	US-08-875-811-61
22	548	95.0	355	3	US-08-875-811-49
23	548	95.0	355	3	US-08-875-811-57
24	548	95.0	355	3	US-08-875-811-64
25	543	94.1	105	3	US-08-875-811-55
26	543	94.1	105	3	US-08-875-811-24
27	543	94.1	105	3	US-08-875-811-26

28	539	93.4	358	3	US-08-875-811-45
29	539	93.4	365	3	US-08-875-811-53
30	524	90.8	107	3	US-08-875-811-20
31	487	84.4	360	3	US-08-875-811-47
32	480.5	83.3	111	3	US-08-875-811-22
33	442	76.6	83	3	US-08-875-811-2
34	442	76.6	83	4	US-09-071-672-3
35	286	49.6	111	2	US-08-891-848-12
36	286	49.6	111	3	US-08-875-811-8
37	214.5	37.2	114	3	US-09-223-118-4
38	202.5	35.1	114	3	US-09-223-118-2
39	201.5	34.9	114	3	US-09-223-118-1
40	199.5	34.6	114	3	US-09-223-118-3
41	156.5	27.1	169	1	US-08-441-629-2
42	156.5	27.1	169	3	US-08-776-207-2
43	156.5	27.1	169	4	US-09-507-773-2
44	156.5	27.1	169	5	PCT-US95-09172-2
45	143	24.8	28	3	US-08-875-811-3

ALIGNMENTS

RESULT 1
US-08-467-955-2
Sequence 2, Application US/08467955
Patent No. 5728605
GENERAL INFORMATION:
APPLICANT: Ardelt Ph.D, Wojciech J.
TITLE OF INVENTION: PHARMACEUTICALS AND METHOD FOR MAKING THEM
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mark H. Jay, P.A.
STREET: P.O. Box E
CITY: Short Hills
STATE: New Jersey
COUNTRY: USA
ZIP: 07078-0283
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,955
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/178,118
FILING DATE: 06-APR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/436,141
FILING DATE: 13-NOV-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/814,332
FILING DATE: 03-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/283,970
FILING DATE: 01-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Jay, Mark H.
REGISTRATION NUMBER: 27507
REFERENCE/DOCKET NUMBER: 5007 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-912-9066
TELEFAX: 201-912-0442
TELEX: No. 5728605 Applicable
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 104 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: protein
HYPOTHETICAL: N
ANTI-SENSE: N
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Rana pipiens
DEVELOPMENTAL STAGE: Oocyte
US-08-467-955-2

Query Match 96.2%; Score 553; DB 1; Length 104;
Best Local Similarity 95.2%; Pred. No. 2.4e-60;
Matches 99; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ODMLTFOKKHLTNTRDVCNNILSTNLFHCKDKNTFIYSRPPVKAICKGIASKNVLT 60
Db 1 EDMLTFOKKHVTNTRDVCNNIMSTNLFHCKDKNTFIYSRPPVKAICKGIASKNVLT 60
Qy 61 SEFYISDCNVTSRPCKYKTKKSTNFCVTCENQAPVHFVGSHC 104
Db 61 SEFYISDCNVTSRPCKYKTKKSTNFCVTCENQAPVHFVGSHC 104

RESULT 2

US-09-394-268-1
Sequence 1, Application US/09394268
Patent No. 6175003
GENERAL INFORMATION:
APPLICANT: Saxena, Shaileendra K
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING RIBONUCLEASES AND METHODS OF
TITLE OF INVENTION: MAKING THEM
FILE REFERENCE: 5013
CURRENT APPLICATION NUMBER: US/09/394,268
CURRENT FILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 104
TYPE: PRT
ORGANISM: Rana pipiens
US-09-394-268-1

Query Match 95.8%; Score 553; DB 3; Length 104;
Best Local Similarity 95.2%; Pred. No. 4.1e-60;
Matches 99; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ODMLTFOKKHLTNTRDVCNNILSTNLFHCKDKNTFIYSRPPVKAICKGIASKNVLT 60
Db 1 ODMLTFOKKHVTNTRDVCNNIMSTNLFHCKDKNTFIYSRPPVKAICKGIASKNVLT 60
Qy 61 SEFYISDCNVTSRPCKYKTKKSTNFCVTCENQAPVHFVGSHC 104
Db 61 SEFYISDCNVTSRPCKYKTKKSTNFCVTCENQAPVHFVGSHC 104

RESULT 3

US-09-687-748-1
Sequence 1, Application US/09687748
Patent No. 6423515
GENERAL INFORMATION:
APPLICANT: Saxena, Shaileendra K
TITLE OF INVENTION: METHODS OF MAKING NUCLEIC ACIDS ENCODING RIBONUCLEASES
FILE REFERENCE: 5013 US 01
CURRENT APPLICATION NUMBER: US/09/687,748
CURRENT FILING DATE: 2000-10-14
PRIOR APPLICATION NUMBER: 09/394,268
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 104
TYPE: PRT
ORGANISM: Rana pipiens
US-09-687-748-1

Query Match 95.8%; Score 553; DB 4; Length 104;
Best Local Similarity 95.2%; Pred. No. 4.1e-60;
Matches 99; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ODMLTFOKKHLTNTRDVCNNILSTNLFHCKDKNTFIYSRPPVKAICKGIASKNVLT 60
Db 1 ODMLTFOKKHVTNTRDVCNNIMSTNLFHCKDKNTFIYSRPPVKAICKGIASKNVLT 60
Qy 61 SEFYISDCNVTSRPCKYKTKKSTNFCVTCENQAPVHFVGSHC 104
Db 61 SEFYISDCNVTSRPCKYKTKKSTNFCVTCENQAPVHFVGSHC 104

RESULT 4

US-08-875-811-63
Sequence 63, Application US/08875811
Patent No. 6045793
GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Boque, Luis
APPLICANT: Wlodawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Paris, Susan K.
REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 015280-244100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 129 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-875-811-63

Query Match 95.8%; Score 553; DB 3; Length 129;
Best Local Similarity 95.2%; Pred. No. 5.5e-60;
Matches 99; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ODMLTFOKKHLTNTRDVCNNILSTNLFHCKDKNTFIYSRPPVKAICKGIASKNVLT 60
Db 26 ODMLTFOKKHVTNTRDVCNNIMSTNLFHCKDKNTFIYSRPPVKAICKGIASKNVLT 85
Qy 61 SEFYISDCNVTSRPCKYKTKKSTNFCVTCENQAPVHFVGSHC 104
Db 86 SEFYISDCNVTSRPCKYKTKKSTNFCVTCENQAPVHFVGSHC 129

RESULT 5
US-08-875-811-43
Sequence 43, Application US/08875811
Patent No. 6045793
GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Boque, Luis
APPLICANT: Wlodawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Paris, Susan K.
REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 015280-244100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 379 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-875-811-43

Query Match 95.8%; Score 553; DB 3; Length 379;
Best Local Similarity 95.2%; Pred. No. 2.3e-59;
Matches 99; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 QDWLTFQKHLTNRDVCNNILSTNLFHCKDKNTFIYSRPEPVKAIKGIASKNVLT 60
DB 26 QDWLTFQKHLTNRDVCNNILSTNLFHCKDKNTFIYSRPEPVKAIKGIASKNVLT 85
QY 61 SEFLSDCVNTSRPCKYKLLKSTNTFCVTCENQAPVHFVGHC 104
DB 86 SEFLSDCVNTSRPCKYKLLKSTNTFCVTCENQAPVHFVGSC 129

RESULT 6
US-08-283-971-1
Sequence 1, Application US/08283971
Patent No. 5529775
GENERAL INFORMATION:
APPLICANT: Ardelit Ph.D, Wojciech J.
APPLICANT: Mikulski, Stanislaw M.
TITLE OF INVENTION: PHARMACEUTICAL FOR TREATING TUMORS IN HUMANS
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:

ADDRESSEE: Mark H. Jay, P.C.
STREET: P.O. Box 020083, General Post Office
CITY: Brooklyn
STATE: New York
COUNTRY: USA
ZIP: 11202-0002
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/283,971
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/921,180
FILING DATE: 30-JUL-1992
APPLICATION NUMBER: US 07/178,118
FILING DATE: 06-APR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/436,141
FILING DATE: 13-NOV-1989
ATTORNEY/AGENT INFORMATION:
NAME: Jay, Mark H.
REGISTRATION NUMBER: 27507
REFERENCE/DOCKET NUMBER: 5006 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 718-625-0399
TELEFAX: 718-625-0399
TEXT: No. 5529775, Applicable
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 104 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: N
ANTI-SENSE: N
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Rana pipiens
DEVELOPMENTAL STAGE: Embryo
US-08-283-971-1

Query Match 95.3%; Score 550; DB 1; Length 104;
Best Local Similarity 94.2%; Pred. No. 9.6e-60;
Matches 98; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 QDWLTFQKHLTNRDVCNNILSTNLFHCKDKNTFIYSRPEPVKAIKGIASKNVLT 60
DB 1 EDWLTFQKHLTNRDVCNNILSTNLFHCKDKNTFIYSRPEPVKAIKGIASKNVLT 60
QY 61 SEFLSDCVNTSRPCKYKLLKSTNTFCVTCENQAPVHFVGHC 104
DB 61 SEFLSDCVNTSRPCKYKLLKSTNTFCVTCENQAPVHFVGSC 104

RESULT 7
US-07-921-619-1
Sequence 1, Application US/07921619
Patent No. 5595734
GENERAL INFORMATION:
APPLICANT: Ardelit Ph.D, Wojciech J.
APPLICANT: Mikulski, Stanislaw M.
TITLE OF INVENTION: PHARMACEUTICAL FOR TREATING TUMORS IN HUMANS
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mark H. Jay, P.C.
STREET: P.O. Box 020083, General Post Office
CITY: Brooklyn
STATE: New York

COUNTRY: USA
ZIP: 11202-0002
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/921,619
FILING DATE: 19920728
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/178,118
FILING DATE: 06-APR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/436,141
FILING DATE: 13-NOV-1989
ATTORNEY/AGENT INFORMATION:
NAME: Jay, Mark H.
REGISTRATION NUMBER: 27507
REFERENCE/DOCKET NUMBER: 5005 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 718-625-0399
TELEFAX: 718-625-0399
TELEX: No. 5595734 Applicable
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 104 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: N
ANTI-SENSE: N
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Rana pipiens
DEVELOPMENTAL STAGE: Embryo
US-07-921-619-1

Query Match 95.3%; Score 550; DB 1; Length 104;
Best Local Similarity 94.2%; Pred. No. 9.6e-60;
Matches 98; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
QY 1 ODMLTFQKXHLTNRDVDCNNILSTNLFPHCKDKXNTFTYSRPPVPAICGIIASKNVLT 60
DB 1 EDMLTFQKXHLTNRDVDCNNILSTNLFPHCKDKXNTFTYSRPPVPAICGIIASKNVLT 60
QY 61 SEFYISDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 104
DB 61 SEFYISDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGSC 104

RESULT 8
US-08-467-955-1
Sequence 1, Application US/08467955
Patent No. 5728805
GENERAL INFORMATION:
APPLICANT: Atdele P.D. Wojciech J.
TITLE OF INVENTION: PHARMACEUTICALS AND METHOD FOR MAKING THEM
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Mark H. Jay, P.A.
STREET: P.O. Box E
CITY: Short Hills
STATE: New Jersey
COUNTRY: USA
ZIP: 07078-0383
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,955
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/178,118
FILING DATE: 06-APR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/436,141
FILING DATE: 13-NOV-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/814,332
FILING DATE: 03-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/283,970
FILING DATE: 01-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Jay, Mark H.
REGISTRATION NUMBER: 27507
REFERENCE/DOCKET NUMBER: 5007 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-912-9066
TELEFAX: 201-912-0442
TELEX: No. 5728805 Applicable
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 104 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHEICAL: N
ANTI-SENSE: N
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Rana pipiens
DEVELOPMENTAL STAGE: Oocyte
US-08-467-955-1

Query Match 95.3%; Score 550; DB 1; Length 104;
Best Local Similarity 94.2%; Pred. No. 9.6e-60;
Matches 98; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
QY 1 ODMLTFQKXHLTNRDVDCNNILSTNLFPHCKDKXNTFTYSRPPVPAICGIIASKNVLT 60
DB 1 EDMLTFQKXHLTNRDVDCNNILSTNLFPHCKDKXNTFTYSRPPVPAICGIIASKNVLT 60
QY 61 SEFYISDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 104
DB 61 SEFYISDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGSC 104

RESULT 9
US-08-891-848-13
Sequence 13, Application US/08891848
Patent No. 5955073
GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Youle, Richard J.
APPLICANT: Newton, Dianne L.
APPLICANT: Nicholls, Peter J.
TITLE OF INVENTION: Selective RNase Cytotoxic Reagents
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/891,848
FILING DATE: No. 5955073 yet assigned
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/125,462
FILING DATE: 22-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/014,082
FILING DATE: 04-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/779,195
FILING DATE: 22-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/510,696
FILING DATE: 20-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 015280-110310US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 104 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..104
OTHER INFORMATION: /label= Onc
US-08-891-848-13

Query Match      95.3%; Score 550; DB 2; Length 104;
Best Local Similarity 94.2%; Pred. No. 9.6e-60;
Matches 98; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 QDWLTFQKHLTNTRDVCNNILSTNLFPHCKDKNTFTYSRPEPVAKICKGIIASKNVLT 60
DB 1 QDWLTFQKHLTNTRDVCNNILSTNLFPHCKDKNTFTYSRPEPVAKICKGIIASKNVLT 60
QY 61 SEFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 104
DB 61 SEFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGSC 104

RESULT 10
US-09-394-268-2
Sequence 2, Application US/09394268
Patent No. 6175003
GENERAL INFORMATION:
APPLICANT: Saxena, Shaileendra K
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING RIBONUCLEASES AND METHODS OF
FILE REFERENCE: 5013
CURRENT APPLICATION NUMBER: US/09/394,268
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 104
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: SEQ ID NO:1 with Leu at position 23 and Cys at
US-09-394-268-2
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Query Match      95.3%; Score 550; DB 3; Length 104;
Best Local Similarity 95.2%; Pred. No. 9.6e-60;
Matches 99; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 QDWLTFQKHLTNTRDVCNNILSTNLFPHCKDKNTFTYSRPEPVAKICKGIIASKNVLT 60
DB 1 QDWLTFQKHLTNTRDVCNNILSTNLFPHCKDKNTFTYSRPEPVAKICKGIIASKNVLT 60
QY 61 SEFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 104
DB 61 SEFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGSC 104

RESULT 11
US-09-687-748-2
Sequence 2, Application US/09687748
Patent No. 6423515
GENERAL INFORMATION:
APPLICANT: Saxena, Shaileendra K
TITLE OF INVENTION: METHODS OF MAKING NUCLEIC ACIDS ENCODING RIBONUCLEASES
FILE REFERENCE: 5013 US 01
CURRENT APPLICATION NUMBER: US/09/687,748
CURRENT FILING DATE: 2000-10-14
PRIOR APPLICATION NUMBER: 09/394,268
PRIOR FILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 104
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: SEQ ID NO:1 with Leu at position 23 and Cys at
US-09-687-748-2

Query Match      95.3%; Score 550; DB 4; Length 104;
Best Local Similarity 95.2%; Pred. No. 9.6e-60;
Matches 99; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 QDWLTFQKHLTNTRDVCNNILSTNLFPHCKDKNTFTYSRPEPVAKICKGIIASKNVLT 60
DB 1 QDWLTFQKHLTNTRDVCNNILSTNLFPHCKDKNTFTYSRPEPVAKICKGIIASKNVLT 60
QY 61 SEFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 104
DB 61 SEFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGSC 104

RESULT 12
US-08-875-811-39
Sequence 39, Application US/08875811
Patent No. 6045793
GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Bogue, Lluvia
APPLICANT: Wlodawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875, 811
FILING DATE: 19-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Paris, Susan K.
REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 015280-244100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 105 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-875-811-39

Query Match 95.3%; Score 550; DB 3; Length 105;
Best Local Similarity 94.2%; Pred. No. 9,7e-60;
Matches 98; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ODMLTFQKKHLTNTDVCNNILSTNLFPHCKDKNTFYSRPPVPAICGIIASKNVLT 60
Db 2 EDMLTFQKKHLTNTDVCNNILSTNLFPHCKDKNTFYSRPPVPAICGIIASKNVLT 61
Qy 61 SEFYSDCNVTSRPPCKYKLKKSNTFCVTCENQAPVHFVGSHC 104
Db 62 SEFYSDCNVTSRPPCKYKLKKSNTKFCVTCENQAPVHFVGSC 105

RESULT 13
US-08-875-811-41
Sequence 41, Application US/08875811
Patent No. 6045793
GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Boque, Luis
APPLICANT: Wlodawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875, 811
FILING DATE: 19-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Paris, Susan K.

REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 015280-244100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-875-811-41

Query Match 95.3%; Score 550; DB 3; Length 355;
Best Local Similarity 94.2%; Pred. No. 4,8e-59;
Matches 98; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ODMLTFQKKHLTNTDVCNNILSTNLFPHCKDKNTFYSRPPVPAICGIIASKNVLT 60
Db 252 EDMLTFQKKHLTNTDVCNNILSTNLFPHCKDKNTFYSRPPVPAICGIIASKNVLT 311
Qy 61 SEFYSDCNVTSRPPCKYKLKKSNTFCVTCENQAPVHFVGSHC 104
Db 312 SEFYSDCNVTSRPPCKYKLKKSNTKFCVTCENQAPVHFVGSC 355

RESULT 14
US-08-875-811-51
Sequence 51, Application US/08875811
Patent No. 6045793
GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Boque, Luis
APPLICANT: Wlodawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875, 811
FILING DATE: 19-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Paris, Susan K.
REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 015280-244100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 358 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-875-811-51

Query Match 95.3%; Score 550; DB 3; Length 358;
Best Local Similarity 94.2%; Pred. No. 4.9e-59;
Matches 98; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

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QY 61 SEFYLSDCNVTSRPCRYKLLKSTNTFCVTCENQAPVHFGVGHG 104
DB 62 SEFYLSDCNVTSRPCRYKLLKSTNTFCVTCENQAPVHFGVGHG 105

RESULT 15

US-08-875-811-1
Sequence 1, Application US/08875811
Patent No. 6045793
GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Bogue, Luis
APPLICANT: Wlodaver, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Fairis, Susan K.
REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 015280-244100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 104 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..104
OTHER INFORMATION: /label= "nonc
OTHER INFORMATION: /note= "native ONCONASE (Registered
OTHER INFORMATION: Trademark) from Rana pipiens"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: /note= "Xaa = pyroglutamic acid"
US-08-875-811-1

Query Match 95.0%; Score 548; DB 3; Length 104;
Best Local Similarity 95.1%; Pred. No. 1.7e-59;
Matches 98; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 DMLTFQKGLTNTRDVDCNNILSTNLFHCKDKNTFIYSRPEPVKAICKGIASKNVLT 61
DB 2 DMLTFQKGIITNTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIASKNVLT 61
QY 62 EFLYSDCNVTSRPCRYKLLKSTNTFCVTCENQAPVHFGVGHG 104
DB 62 EFLYSDCNVTSRPCRYKLLKSTNTFCVTCENQAPVHFGVGHG 104

Search completed: January 22, 2004, 12:10:06
Job time: 13.4644 secs

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OM protein - protein search, using sw model

Run on: January 22, 2004, 12:02:15 ; Search time 24.7341 Seconds

(without alignments)
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Title: US-09-622-613c-4

Perfect score: 577
Sequence: 1 QDWLTFQKHLLTNTRDVDCN.....TFCVTCENQAPVHFVGHC 104

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 777136 segs, 206736638 residues

Total number of hits satisfying chosen parameters: 777136

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA:*

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- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
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- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	575	99.7	105	11	US-09-961-400-6
5	575	99.7	127	11	US-09-948-391A-28
6	575	99.7	127	11	US-09-961-400-28
7	571	99.0	104	11	US-09-948-391A-4
8	571	99.0	104	11	US-09-961-400-4
9	570	98.8	104	11	US-09-948-391A-11
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17	553	95.8	105	15	US-10-153-882-2	Sequence 2, Appli
18	548	95.0	104	10	US-09-966-119-1	Sequence 1, Appli
19	548	95.0	104	11	US-09-918-887-1	Sequence 1, Appli
20	442	76.6	83	10	US-09-966-119-3	Sequence 3, Appli
21	442	76.6	83	11	US-09-918-887-3	Sequence 3, Appli
22	279.5	48.4	110	11	US-09-961-400-19	Sequence 19, Appli
23	279.5	48.4	111	11	US-09-948-391A-21	Sequence 21, Appli
24	279.5	48.4	111	11	US-09-961-400-21	Sequence 21, Appli
25	279.5	48.4	117	11	US-09-948-391A-22	Sequence 22, Appli
26	279.5	48.4	117	11	US-09-961-400-22	Sequence 22, Appli
27	278.5	48.3	110	11	US-09-948-391A-15	Sequence 15, Appli
28	278.5	48.3	110	11	US-09-961-400-15	Sequence 15, Appli
29	278.5	48.3	111	11	US-09-961-400-17	Sequence 17, Appli
30	273.5	47.4	110	11	US-09-948-391A-19	Sequence 19, Appli
31	273.5	47.4	110	11	US-09-948-391A-24	Sequence 24, Appli
32	273.5	47.4	110	11	US-09-961-400-24	Sequence 24, Appli
33	273.5	47.4	111	11	US-09-948-391A-26	Sequence 26, Appli
34	273.5	47.4	111	11	US-09-961-400-26	Sequence 26, Appli
35	272.5	47.2	111	11	US-09-948-391A-17	Sequence 17, Appli
36	156.5	27.1	169	13	US-10-016-447-2	Sequence 13, Appli
37	146	25.3	119	12	US-10-074-978A-139	Sequence 139, App
38	125.5	21.8	124	13	US-10-016-447-5	Sequence 5, Appli
39	112	19.4	147	9	US-09-286-240-6	Sequence 6, Appli
40	112	19.4	147	9	US-09-863-777-2	Sequence 2, Appli
41	112	19.4	147	10	US-09-731-872-254	Sequence 254, App
42	112	19.4	147	12	US-09-876-997-254	Sequence 254, App
43	109	18.9	124	10	US-09-981-286A-8	Sequence 8, Appli
44	103.5	17.9	99	12	US-10-074-978A-141	Sequence 141, App
45	101.5	17.6	89	12	US-10-074-978A-143	Sequence 143, App

ALIGNMENTS

RESULT 1
US-09-961-400-9
Sequence 9, Application US/09961400
Publication No. US20030124131A1
GENERAL INFORMATION:
APPLICANT: RYBAK, SUSANNA M.
APPLICANT: GOLDENBERG, DAVID M.
APPLICANT: NEWTON, DIANNE L.
TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
FILE REFERENCE: 018733/1059
CURRENT FILING DATE: 2001-09-25
PRIOR FILING DATE: 2000-08-17
PRIOR APPLICATION NUMBER: 09/622,613
PRIOR FILING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: 60/079,751
PRIOR FILING DATE: 1998-03-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 9
LENGTH: 111
TYPE: PRT
ORGANISM: Rana pipiens
US-09-961-400-9
Query Match: 100.0%; Score 577; DB 11; Length 111;
Best Local Similarity 100.0%; Pred. No. 2.4e-58;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 61 SEFYLSDCNVTSRPCKYKLLKKSSTFTFCVTCENQAPVHFVGHC 104
68 SEFYLSDCNVTSRPCKYKLLKKSSTFTFCVTCENQAPVHFVGHC 111

RESULT 2
US-09-961-400-2
; Sequence 2, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: GOLDENBERG, DAVID M.
; APPLICANT: NEWTON, DIANNE L.
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 018733/1059
; CURRENT APPLICATION NUMBER: US/09/961,400
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 09/622,613
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/079,751
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 104
; TYPE: PRT
; ORGANISM: Rana pipiens
US-09-961-400-2

Query Match 99.7%; Score 575; DB 11; Length 104;
Best Local Similarity 99.0%; Pred. No. 3.8e-58;
Matches 103; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QDMLTFQKHLNTRDVCNNILSTNLFPHCKDKNTFYSRPPVKAICKGIIASKNVLT 60
DB 1 QDMLTFQKHLNTRDVCNNILSTNLFPHCKDKNTFYSRPPVKAICKGIIASKNVLT 60

QY 61 SEFYISDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 104
DB 61 SEFYISDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 104

RESULT 3
US-09-948-391A-6
; Sequence 6, Application US/09948391A
; Publication No. US20030027311A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: NEWTON, DIANNE L.
; APPLICANT: The United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Recombinant Anti-Tumor RNase
; FILE REFERENCE: 015280-343110US
; CURRENT APPLICATION NUMBER: US/09/948,391A
; CURRENT FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 60/079,751
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/622,613
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Rana pipiens
; OTHER INFORMATION: ribonuclease with Met at position 1 (recombinant
; OTHER INFORMATION: Met(-1) RapLRI)
US-09-948-391A-6

Query Match 99.7%; Score 575; DB 11; Length 105;
Best Local Similarity 99.0%; Pred. No. 3.9e-58;
Matches 103; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QDMLTFQKHLNTRDVCNNILSTNLFPHCKDKNTFYSRPPVKAICKGIIASKNVLT 60
DB 2 QDMLTFQKHLNTRDVCNNILSTNLFPHCKDKNTFYSRPPVKAICKGIIASKNVLT 61

QY 61 SEFYISDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 104
DB 62 SEFYISDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 105

RESULT 4
US-09-961-400-6
; Sequence 6, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: GOLDENBERG, DAVID M.
; APPLICANT: NEWTON, DIANNE L.
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 018733/1059
; CURRENT APPLICATION NUMBER: US/09/961,400
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 09/622,613
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/079,751
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Rana pipiens
US-09-961-400-6

Query Match 99.7%; Score 575; DB 11; Length 105;
Best Local Similarity 99.0%; Pred. No. 3.9e-58;
Matches 103; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QDMLTFQKHLNTRDVCNNILSTNLFPHCKDKNTFYSRPPVKAICKGIIASKNVLT 60
DB 2 QDMLTFQKHLNTRDVCNNILSTNLFPHCKDKNTFYSRPPVKAICKGIIASKNVLT 61

QY 61 SEFYISDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 104
DB 62 SEFYISDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 105

RESULT 5
US-09-948-391A-28
; Sequence 28, Application US/09948391A
; Publication No. US20030027311A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: NEWTON, DIANNE L.
; APPLICANT: The United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Recombinant Anti-Tumor RNase
; FILE REFERENCE: 015280-343110US
; CURRENT APPLICATION NUMBER: US/09/948,391A
; CURRENT FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 60/079,751
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/622,613

PRIOR FILING DATE: 2000-08-17
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 28
LENGTH: 127
TYPE: PRT
ORGANISM: Rana pipiens
FEATURE:
OTHER INFORMATION: Rana pipiens ribonuclease (RaplR1) clone 5a1b cDNA
US-09-948-391A-28

Query Match 99.7%; Score 575; DB 11; Length 127;
Best Local Similarity 99.0%; Pred. No. 4.8e-58;
Matches 103; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QDWLTFQKHLNTRDVCNNILSTNLFHCKDKNTFIYSRPPVKAICKGIIASKNVLT 60
DB 24 QDWLTFQKHLNTRDVCNNIMSTNLFHCKDKNTFIYSRPPVKAICKGIIASKNVLT 83
QY 61 SEFYISDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGHC 104
DB 84 SEFYISDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGHC 127

RESULT 6
US-09-961-400-28
Sequence 28, Application US/09961400
Publication No. US20030124131A1
GENERAL INFORMATION:
APPLICANT: RYBAK, SUSANNA M.
APPLICANT: GOLDBERG, DAVID M.
APPLICANT: NEWTON, DIANNE L.
TITLE OF INVENTION: IMMUNOCOMUNGATES OF TOXINS DIRECTED AGAINST MALIGNANT
FILE REFERENCE: 018733/1059
CURRENT APPLICATION NUMBER: US/09/961,400
CURRENT FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: 09/622,613
PRIOR FILING DATE: 2000-08-17
PRIOR APPLICATION NUMBER: PCT/US99/06641
PRIOR FILING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: 60/079,751
PRIOR FILING DATE: 1998-03-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 28
LENGTH: 127
TYPE: PRT
ORGANISM: Rana pipiens
US-09-961-400-28

Query Match 99.7%; Score 575; DB 11; Length 127;
Best Local Similarity 99.0%; Pred. No. 4.8e-58;
Matches 103; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QDWLTFQKHLNTRDVCNNILSTNLFHCKDKNTFIYSRPPVKAICKGIIASKNVLT 60
DB 24 QDWLTFQKHLNTRDVCNNIMSTNLFHCKDKNTFIYSRPPVKAICKGIIASKNVLT 83
QY 61 SEFYISDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGHC 104
DB 84 SEFYISDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGHC 127

RESULT 7
US-09-948-391A-4
Sequence 4, Application US/09948391A
Publication No. US20030027311A1
GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: The United States of America

APPLICANT: as represented by The Secretary of the
Department of Health and Human Services
TITLE OF INVENTION: Recombinant Anti-Tumor RNase
FILE REFERENCE: 015280-343110US
CURRENT APPLICATION NUMBER: US/09/948,391A
CURRENT FILING DATE: 2002-05-10
PRIOR APPLICATION NUMBER: US 60/079,751
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: WO PCT/US99/06641
PRIOR FILING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: US 09/622,613
PRIOR FILING DATE: 2000-08-17
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4
LENGTH: 104
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Rana pipiens
OTHER INFORMATION: ribonuclease with Met23Leu substitution
OTHER INFORMATION: (recombinant RaplR1 Met23Leu)
US-09-948-391A-4

Query Match 99.0%; Score 571; DB 11; Length 104;
Best Local Similarity 99.0%; Pred. No. 1.1e-57;
Matches 103; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QDWLTFQKHLNTRDVCNNILSTNLFHCKDKNTFIYSRPPVKAICKGIIASKNVLT 60
DB 1 QDWLTFQKHLNTRDVCNNILSTNLFHCKDKNTFIYSRPPVKAICKGIIASKNVLT 60
QY 61 SEFYISDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGHC 104
DB 61 SEFYISDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGHC 104

RESULT 8
US-09-961-400-4
Sequence 4, Application US/09961400
Publication No. US20030124131A1
GENERAL INFORMATION:
APPLICANT: RYBAK, SUSANNA M.
APPLICANT: GOLDBERG, DAVID M.
APPLICANT: NEWTON, DIANNE L.
TITLE OF INVENTION: IMMUNOCOMUNGATES OF TOXINS DIRECTED AGAINST MALIGNANT
FILE REFERENCE: 018733/1059
CURRENT APPLICATION NUMBER: US/09/961,400
CURRENT FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: 09/622,613
PRIOR FILING DATE: 2000-08-17
PRIOR APPLICATION NUMBER: PCT/US99/06641
PRIOR FILING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: 60/079,751
PRIOR FILING DATE: 1998-03-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 104
TYPE: PRT
ORGANISM: Rana pipiens
US-09-961-400-4

Query Match 99.0%; Score 571; DB 11; Length 104;
Best Local Similarity 99.0%; Pred. No. 1.1e-57;
Matches 103; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QDWLTFQKHLNTRDVCNNILSTNLFHCKDKNTFIYSRPPVKAICKGIIASKNVLT 60
DB 1 QDWLTFQKHLNTRDVCNNILSTNLFHCKDKNTFIYSRPPVKAICKGIIASKNVLT 60
QY 61 SEFYISDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGHC 104

DB 61 EFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVC 104

RESULT 9
US-09-948-391A-11

Sequence 11, Application US/09948391A
Publication No. US20030027311A1
GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Diane L.
APPLICANT: The United States of America
APPLICANT: as represented by The Secretary of the
Department of Health and Human Services
TITLE OF INVENTION: Recombinant Anti-Tumor RNase
FILE REFERENCE: 015280-343110US
CURRENT APPLICATION NUMBER: US/09/948,391A
CURRENT FILING DATE: 2002-05-10
PRIOR APPLICATION NUMBER: US 60/079,751
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: WO PCT/US99/06641
PRIOR FILING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: US 09/622,613
PRIOR FILING DATE: 2000-08-17
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 11
LENGTH: 104
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Rana pipiens
OTHER INFORMATION: ribonuclease with Glu1ser substitution
OTHER INFORMATION: (recombinant RapiR1 Q1S)
US-09-948-391A-11

Query Match 98.8%; Score 570; DB 11; Length 104;
Best Local Similarity 99.0%; Pred. No. 1.4e-57;
Matches 102; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWLTFQKHLTNTRDVCNNILSTNLFHCKDKNTFYSRPEPVKAICKGIIASKNVLTTS 61
DB 2 DWLTFQKHLTNTRDVCNNIMSTNLFHCKDKNTFYSRPEPVKAICKGIIASKNVLTTS 61

QY 62 EFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVC 104
DB 62 EFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVC 104

RESULT 10
US-09-961-400-11

Sequence 11, Application US/09961400
Publication No. US20030124131A1
GENERAL INFORMATION:
APPLICANT: RYBAK, SUSANNA M.
APPLICANT: GOLDENBERG, DAVID M.
APPLICANT: NEWTON, DIANNE L.
TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
FILE REFERENCE: 018733/1059
CURRENT APPLICATION NUMBER: US/09/961,400
CURRENT FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: 09/622,613
PRIOR FILING DATE: 2000-08-17
PRIOR APPLICATION NUMBER: PCT/US99/06641
PRIOR FILING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: 60/079,751
PRIOR FILING DATE: 1998-03-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 11
LENGTH: 104
TYPE: PRT

ORGANISM: Rana pipiens
US-09-961-400-11

Query Match 98.8%; Score 570; DB 11; Length 104;
Best Local Similarity 99.0%; Pred. No. 1.4e-57;
Matches 102; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWLTFQKHLTNTRDVCNNILSTNLFHCKDKNTFYSRPEPVKAICKGIIASKNVLTTS 61
DB 2 DWLTFQKHLTNTRDVCNNIMSTNLFHCKDKNTFYSRPEPVKAICKGIIASKNVLTTS 61

QY 62 EFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVC 104
DB 62 EFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVC 104

RESULT 11
US-09-948-391A-13

Sequence 13, Application US/09948391A
Publication No. US20030027311A1
GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Diane L.
APPLICANT: The United States of America
APPLICANT: as represented by The Secretary of the
Department of Health and Human Services
TITLE OF INVENTION: Recombinant Anti-Tumor RNase
FILE REFERENCE: 015280-343110US
CURRENT APPLICATION NUMBER: US/09/948,391A
CURRENT FILING DATE: 2002-05-10
PRIOR APPLICATION NUMBER: US 60/079,751
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: WO PCT/US99/06641
PRIOR FILING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: US 09/622,613
PRIOR FILING DATE: 2000-08-17
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 13
LENGTH: 105
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Rana pipiens
OTHER INFORMATION: ribonuclease with Met at position 1 and Glu1Ser
OTHER INFORMATION: substitution (recombinant Met(-1) RapiR1 Q1S)
US-09-948-391A-13

Query Match 98.8%; Score 570; DB 11; Length 105;
Best Local Similarity 99.0%; Pred. No. 1.4e-57;
Matches 102; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 DWLTFQKHLTNTRDVCNNILSTNLFHCKDKNTFYSRPEPVKAICKGIIASKNVLTTS 61
DB 3 DWLTFQKHLTNTRDVCNNIMSTNLFHCKDKNTFYSRPEPVKAICKGIIASKNVLTTS 62

QY 62 EFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVC 104
DB 63 EFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVC 105

RESULT 12
US-09-961-400-13

Sequence 13, Application US/09961400
Publication No. US20030124131A1
GENERAL INFORMATION:
APPLICANT: RYBAK, SUSANNA M.
APPLICANT: GOLDENBERG, DAVID M.
APPLICANT: NEWTON, DIANNE L.
TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
FILE REFERENCE: 018733/1059
CURRENT APPLICATION NUMBER: US/09/961,400

CURRENT FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: 09/622,613
PRIOR FILING DATE: 2000-08-17
PRIOR APPLICATION NUMBER: PCT/US99/06641
PRIOR FILING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: 60/079,751
PRIOR FILING DATE: 1998-03-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 13
LENGTH: 105
TYPE: PRT
ORGANISM: Rana pipiens
US-09-961-400-13

Query Match 98.8%; Score 570; DB 11; Length 105;
Best Local Similarity 99.0%; Pred. No. 1,4e-57;
Matches 102; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 DMLTFQKXHLNTRVDVDCNNILSTNLFHCKDKNTFTYSRPPVPAICKGIIASKNVLTTS 61
DB 3 DMLTFQKXHLNTRVDVDCNNIMSTNLFHCKDKNTFTYSRPPVPAICKGIIASKNVLTTS 62

OY 62 EFYLSDCNVTSRPCKYKLLKKSNTFCVTCENQAPVHFVGSHC 104
DB 63 EFYLSDCNVTSRPCKYKLLKKSNTFCVTCENQAPVHFVGSHC 105

RESULT 13

US-09-961-400-8
Sequence 8, Application US/09961400
Publication No. US20030124131A1
GENERAL INFORMATION:
APPLICANT: RYBAK, SUSANNA M.
APPLICANT: GOLDENERG, DAVID M.
APPLICANT: NEWTON, DIANNE L.
TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
FILE REFERENCE: 018733/1059
CURRENT APPLICATION NUMBER: US/09/961,400
CURRENT FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: 09/622,613
PRIOR FILING DATE: 2000-08-17
PRIOR APPLICATION NUMBER: PCT/US99/06641
PRIOR FILING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: 60/079,751
PRIOR FILING DATE: 1998-03-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 8
LENGTH: 105
TYPE: PRT
ORGANISM: Rana pipiens
US-09-961-400-8

Query Match 98.3%; Score 567; DB 11; Length 105;
Best Local Similarity 98.1%; Pred. No. 3,2e-57;
Matches 102; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 QDMLTFQKXHLNTRVDVDCNNILSTNLFHCKDKNTFTYSRPPVPAICKGIIASKNVLTTS 60
DB 2 QDMLTFQKXHLNTRVDVDCNNILSTNLFHCKDKNTFTYSRPPVPAICKGIIASKNVLTTS 61

OY 61 SEFYLSDCNVTSRPCKYKLLKKSNTFCVTCENQAPVHFVGSHC 104
DB 62 SEFYLSDCNVTSRPCKYKLLKKSNTFCVTCENQAPVHFVGSHC 105

RESULT 14

US-09-948-391A-2
Sequence 2, Application US/09948391A
Publication No. US20030027311A1
GENERAL INFORMATION:

APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: The United States of America
APPLICANT: as represented by The Secretary of the
Department of Health and Human Services
TITLE OF INVENTION: Recombinant Anti-Tumor RNase
FILE REFERENCE: 015280-343110US
CURRENT APPLICATION NUMBER: US/09/948,391A
CURRENT FILING DATE: 2002-05-10
PRIOR APPLICATION NUMBER: US 60/079,751
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: WO PCT/US99/06641
PRIOR FILING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: US 09/622,613
PRIOR FILING DATE: 2000-08-17
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 104
TYPE: PRT
ORGANISM: Rana pipiens
FEATURE:
OTHER INFORMATION: ribonuclease (RnPLR1)
US-09-948-391A-2

Query Match 98.1%; Score 566; DB 11; Length 104;
Best Local Similarity 98.1%; Pred. No. 4,1e-57;
Matches 102; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 QDMLTFQKXHLNTRVDVDCNNILSTNLFHCKDKNTFTYSRPPVPAICKGIIASKNVLTTS 60
DB 1 QDMLTFQKXHLNTRVDVDCNNIMSTNLFHCKDKNTFTYSRPPVPAICKGIIASKNVLTTS 60

OY 61 SEFYLSDCNVTSRPCKYKLLKKSNTFCVTCENQAPVHFVGSHC 104
DB 61 SEFYLSDCNVTSRPCKYKLLKKSNTFCVTCENQAPVHFVGSHC 104

RESULT 15

US-09-948-391A-8
Sequence 8, Application US/09948391A
Publication No. US20030027311A1
GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: The United States of America
APPLICANT: as represented by The Secretary of the
Department of Health and Human Services
TITLE OF INVENTION: Recombinant Anti-Tumor RNase
FILE REFERENCE: 015280-343110US
CURRENT APPLICATION NUMBER: US/09/948,391A
CURRENT FILING DATE: 2002-05-10
PRIOR APPLICATION NUMBER: US 60/079,751
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: WO PCT/US99/06641
PRIOR FILING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: US 09/622,613
PRIOR FILING DATE: 2000-08-17
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 8
LENGTH: 105
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Rana pipiens
OTHER INFORMATION: ribonuclease with Met at position 1 and Met23Leu
OTHER INFORMATION: substitution (recombinant Met(-1) RnPLR1 Met23Leu)
US-09-948-391A-8

Query Match 97.4%; Score 562; DB 11; Length 105;
Best Local Similarity 98.1%; Pred. No. 1,2e-56;
Matches 102; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy	1	ODWLTFQKGLTNTTRDVCNNILSTNLFHCKDKNTFIYSRPEPVKAICKGIISKXVLT	60
Db	2	ODWLTFQKGLTNTTRDVCNNILSTNLFHCKDKNTFIYSRPEPVKAICKGIISKXVLT	61
Qy	61	SEFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC	104
Db	62	FEFYLSDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC	105

Search completed: January 22, 2004, 12:12:25
Job time : 24.7341 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 22, 2004, 12:01:20 ; Search time 11.6854 Seconds
(without alignments)
855.901 Million cell updates/sec

Title: US-09-622-613C-4
Perfect score: 577
Sequence: 1 ODWLTFOQKXHLTNTRDVDCN.....TFCVTCENQAPVHFVGSHC 104

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	550	95.3	104	2	A39035 ribonuclease-relat
2	286	49.6	111	2	A27121 ribonuclease-relat
3	282.5	49.0	111	1	JX0120 ribonuclease-relat
4	266.5	46.2	111	2	UJ0085 pancreatic ribonuc
5	146	25.3	119	2	S41111 pancreatic ribonuc
6	128	22.2	124	1	NRUI pancreatic ribonuc
7	125	21.7	125	1	A32474 angiotensin [valida
8	123	21.3	128	1	NRCU pancreatic ribonuc
9	122	21.1	124	1	NRMHK pancreatic ribonuc
10	118.5	20.5	145	1	A35932 angiotensin precurs
11	117	20.3	128	1	NRKS angiotensin precurs
12	116	20.1	125	1	B43825 angiotensin - rabbi
13	116	20.1	128	1	NRGPB pancreatic ribonuc
14	114	19.6	124	1	NRVY pancreatic ribonuc
15	113	19.6	128	1	NRVY pancreatic ribonuc
16	112	19.4	147	1	NRHUG angiotensin precurs
17	111	19.2	124	1	NRHP angiotensin - pig
18	109.5	19.0	123	1	A43825 angiotensin - pig
19	109	18.9	124	1	NRBOB pancreatic ribonuc
20	109	18.9	124	1	NRPG pancreatic ribonuc
21	109	18.9	150	1	NRBO pancreatic ribonuc
22	108.5	18.8	147	2	I52489 ribonuclease 4 (EC
23	108	18.7	124	2	S08549 ribonuclease - dom
24	108	18.7	128	1	NRHO pancreatic ribonuc
25	108	18.7	128	1	NRPO pancreatic ribonuc
26	108	18.7	167	2	S20066 pancreatic-type ri
27	107.5	18.6	155	2	JC6159 eosinophil-associat
28	106	18.4	124	1	NRSH pancreatic ribonuc
29	106	18.4	124	1	NRPRH pancreatic ribonuc

30	106	18.4	124	1	NRGPA pancreatic ribonuc
31	106	18.4	124	2	S07141 pancreatic ribonuc
32	105	18.2	124	1	NRWB pancreatic ribonuc
33	105	18.2	124	1	NRGN pancreatic ribonuc
34	104	18.0	124	1	NRGF pancreatic ribonuc
35	104	18.0	156	2	JC6160 eosinophil-associat
36	102	17.7	124	1	NRDEO pancreatic ribonuc
37	102	17.7	124	1	NREKN pancreatic ribonuc
38	102	17.7	124	1	NRGM pancreatic ribonuc
39	102	17.7	124	1	NRGM pancreatic ribonuc
40	102	17.7	124	1	NRMB pancreatic ribonuc
41	102	17.7	124	1	NRW2 pancreatic ribonuc
42	101	17.5	124	1	NRHY pancreatic ribonuc
43	100	17.3	124	1	NRDER pancreatic ribonuc
44	100	17.3	124	1	NRDEN pancreatic ribonuc
45	99	17.2	124	1	NRDEF pancreatic ribonuc

ALIGNMENTS

RESULT 1

A39035

ribonuclease-related anti-tumor protein - northern leopard frog (fragment)

C:Species: Rana pipiens (northern leopard frog)

C>Date: 31-Jul-1991 #sequence_revision 31-Jul-1991 #text_change 30-Jun-1993

C:Accession: A39035

R:Ardelet, W.; Mikulski, S.M.; Shogen, K.

J. Biol. Chem. 266, 245-251, 1991

A:Title: Amino acid sequence of an anti-tumor protein from Rana pipiens oocytes and earl

A:Reference number: A39035; MUID:91093131; PMID:1985896

A:Accession: A39035

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-104 <ARD>

C:Superfamily: pancreatic ribonuclease

Query Match

Best Local Similarity 95.3%; Score 550; DB 2; Length 104;
Matches 98; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy	1	ODWLTFOQKXHLTNTRDVDCNNILSTNLFPHCKDKNTFIYSRPEPVAKIGIIASKNVLT	60
Db	1	EDWLTFOQKXHLTNTRDVDCNNILSTNLFPHCKDKNTFIYSRPEPVAKIGIIASKNVLT	60
Qy	61	SEFYISDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGSHC	104
Db	61	SEFYISDCNVTSRPCKYKLLKSTNTFCVTCENQAPVHFVGSHC	104

RESULT 2

ribonuclease-related sialic acid-binding lectin - bullfrog

C:Species: Rana catesbeiana (bullfrog)

C>Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 30-Jun-1993

C:Accession: A27121

R:Titani, K.; Takio, K.; Kuwada, M.; Nitta, K.; Sakakibara, F.; Kawachi, H.; Takayanagi, Biochemstry 26, 2189-2194, 1987

A:Title: Amino acid sequence of sialic acid-binding lectin from frog (Rana catesbeiana)

A:Reference number: A27121; MUID:67299649; PMID:3304421

A:Accession: A27121

A:Molecule type: protein

A:Residues: 1-111 <TTT>

C:Superfamily: pancreatic ribonuclease

C:Keywords: lectin

Query Match

Best Local Similarity 49.6%; Score 286; DB 2; Length 111;
Matches 53; Conservative 19; Mismatches 32; Indels 8; Gaps 3;

Qy	1	ODWLTFOQKXHLTNTRDVDCNNILSTNLF---HCKDKNTFIYSRPEPVAKIGIIASKNV	56
Db	1	ENWATFOQKHIIINTPIINCNTIMDNNTIYIGGQCKRVTFTIISATVKAICGVI-NMN	59

Qy 57 VLTSEFYSDC---NVTSRPCKYKUKKSTNTFCVTCEAOAPVHFGVGHG 104
Db 60 VLSTRFQNLNCTRTSITRPPCPYSSRTETNYICVACENQYVHFGAGIGRC 110

RESULT 3

JX0120
C:Species: Rana japonica (Japanese frog)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: JX0120
R:Kamaya, Y.; Oyama, F.; Oyama, R.; Sakakibara, F.; Nitta, K.; Kawanishi, H.; Takayanagi, J. Biochem. 108, 139-143, 1990
A:Title: Amino acid sequence of a lectin from Japanese frog (Rana japonica) eggs.
A:Reference number: JX0120; PMID:2229005
A:Accession: JX0120
A:Molecule type: protein
A:Residues: 1-111 <KAM>
A:Experimental source: egg
C:Superfamily: pancreatic ribonuclease
C:Keywords: lectin; pyroglyutamic acid
F:1/Modified site: pyroglutamate carboxylic acid (Gln) #status experimental
F:19-72,34-82,52-97,94-111/Diulfide bonds: #status experimental

Query Match 49.0%; Score 282.5; DB 1; Length 111;
Best Local Similarity 44.1%; Pred. No. 2,2e-21;
Matches 49; Conservative 20; Mismatches 35; Indels 7; Gaps 2;

Qy 1 OQMLTFQKQHLNTRDVCNNILSTNLF---HCKDKNTFYSPRPVPAKIGIASKN 56
Db 1 QWMAFQEGHINTSINCNITMDKSIYVGQCKERNFTIISATVPAKICGSASTNN 60
Qy 57 VLTSEFYSDC---NVTSRPCKYKUKKSTNTFCVTCEAOAPVHFGVGHG 104
Db 61 VLSTRFQNLNCTRTSITRPPCPYSSRTETNYICVACENRLPVHFGAGIGRC 111

RESULT 4

JX0085
C:Species: Rana catesbeiana (bullfrog)
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 05-Aug-1994
C:Accession: JX0085
R:Nitica, R.; Katayama, N.; Okabe, Y.; Iwama, M.; Watanabe, H.; Abe, Y.; Okazaki, T.; Ohguchi, R.; Biochem. 106, 725-735, 1989
A:Title: Primary structure of a ribonuclease from bullfrog (Rana catesbeiana) liver.
A:Reference number: JX0085; PMID:2613682
A:Accession: JX0085
A:Molecule type: protein
A:Residues: 1-111 <NIT>
C:Superfamily: pancreatic ribonuclease
C:Keywords: hydrolase; pyroglyutamic acid
F:1/Modified site: pyroglutamate carboxylic acid (Gln) #status experimental
F:10,35,104/Active site: His, Lys, His #status predicted
F:19-72,34-82,52-97,94-111/Diulfide bonds: #status predicted

Query Match 46.2%; Score 266.5; DB 2; Length 111;
Best Local Similarity 42.3%; Pred. No. 8.8e-20;
Matches 47; Conservative 20; Mismatches 37; Indels 7; Gaps 2;

Qy 1 OQMLTFQKQHLNTRDVCNNILSTNLF---HCKDKNTFYSPRPVPAKIGIASKN 56
Db 1 QWMAFQEGHINTSINCNITMDKSIYVGQCKERNFTIISATVPAKICGSASTNN 60
Qy 57 VLTSEFYSDC---NVTSRPCKYKUKKSTNTFCVTCEAOAPVHFGVGHG 104
Db 61 ELSTTSFKLNTICRISITRPPCPYHSPDDNKLVCACEKQLPVHFGVGHG 111

RESULT 5
S4111
pancreatic ribonuclease - common iguana

C:Species: Iguana iguana (common iguana)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 21-Aug-1998
C:Accession: S4111
R:Zhao, W.; Belintema, J.J.; Hofsteenge, J. Eur. J. Biochem. 219, 641-646, 1994

A:Title: The amino acid sequence of iguana (Iguana iguana) pancreatic ribonuclease.
A:Reference number: S4111; PMID:94139745; PMID:8307028
A:Accession: S4111
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-119 <ZHA>
C:Superfamily: pancreatic ribonuclease

Query Match 25.3%; Score 146; DB 2; Length 119;
Best Local Similarity 29.8%; Pred. No. 1.2e-07;
Matches 34; Conservative 20; Mismatches 44; Indels 16; Gaps 5;

Qy 1 OQMLTFQKQHLNTRDVCNNILSTNLFHCCKDKNTFYSPRPVPAKIC--K 49
Db 1 QWMSFQNKHIDYPTSAISNPVAYCDLMQKRNLPYCKTNTTVAHASPSEIQVCGSG 60
Qy 50 GIASKNVLTSE-FYSDC---NVTSRPCKYKUKKSTNTFCVTCEAOAPVH 98
Db 61 GTHYEDNLVDSNESFDLTDCKNVGGAPSSCKYNGTPTKIRIRACENNQPVH 114

RESULT 6

JNRI
C:Species: Rana catesbeiana (bullfrog)
C:Date: 03-Aug-1984 #sequence_revision 03-Aug-1984 #text_change 04-Oct-1996
C:Accession: A00827
R:Belintema, J.J.; Neuteboom, B. J. Mol. Evol. 19, 145-152, 1983
A:Title: Origin of the duplicated ribonuclease gene in guinea-pig: comparison of the amiA:Reference number: A92957; PMID:87036770; PMID:6571219
A:Accession: A00827
A:Molecule type: protein
A:Residues: 1-124 <BEI>
A:Note: About one-third of the molecules lacked Ala-1
C:Comment: The cula is a rodent belonging to the same subfamily as the guinea pig.
C:Superfamily: pancreatic ribonuclease
C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F:12,11,119/Active site: His, Lys, His #status predicted
F:26-94,40-95,55-110,65-72/Diulfide bonds: #status predicted
F:94/Binding site: carboxylate (Asn) (covalent) #status absent

Query Match 22.2%; Score 128; DB 1; Length 124;
Best Local Similarity 29.8%; Pred. No. 8e-06;
Matches 36; Conservative 19; Mismatches 34; Indels 32; Gaps 7;

Qy 4 LTFQKQHLNTRDVCNNILSTNLFHCCKDKNTFYSPRPVPAKIGIASKN 53
Db 6 MKFQHQHDSGDHPDNTN--YCNEMVVRSMYQGRKRVNPFVHEPLAVQAVC---S 59
Qy 54 SNQV-----LTSFYSDCNVTSRP---CKYKUKKSTNTFCVTCE--OAPVH 97
Db 60 QKNVPCKNGQNTCYOSSHSMRITDCRYTSSRYPCNSYMTAOAKSIIVACGTPSPVH 119

Qy 98 F 98
Db 120 F 120

RESULT 7
A32474
angiogenin [validated] - bovine
N:Alternate names: angiogenesis factor
C:Species: Bos primigenius taurus (cattle)
C:Date: 25-Sep-1989 #sequence_revision 25-Sep-1989 #text_change 15-Sep-2000
C:Accession: A32474; S02001; A30044; S48212

R:Bond, M.D.; Strydom, D.J.
Biochemistry 28, 6110-6113, 1989
A>Title: Amino acid sequence of bovine angiotensin.
A:Reference number: A32474; MUID:89375344; PMID:2757575
A:Accession: A32474
A:Molecule type: protein
A:Residues: 1-125 <BON>
A:Experimental source: plasma
R:Maes, P.; Damer, D.; Rommens, C.; Montreuil, J.; Spik, G.; Tartar, A.
FEBS Lett. 241, 41-45, 1988
A>Title: The complete amino acid sequence of bovine milk angiotensin.
A:Reference number: S02001; MUID:89065101; PMID:3197838
A:Accession: S02001
A:Molecule type: protein
A:Residues: 1-125 <MA>
A:Experimental source: milk
R:Acharya, K.R.; Shapiro, R.; Riordan, J.F.; Vallee, B.L.
submitted to the Brookhaven Protein Data Bank, January 1995
A:Reference number: A65065; PDB:1AGI
A:Contents: annotation; X-ray crystallography, 1.5 angstroms, residues 1-125
R:Acharya, K.R.; Shapiro, R.; Riordan, J.F.; Vallee, B.L.
Proc. Natl. Acad. Sci. U.S.A. 92, 2949-2953, 1995
A>Title: Crystal structure of bovine angiotensin at 1.5 Angstroms resolution.
A:Reference number: A58315; MUID:95224057; PMID:7708754
A:Contents: annotation; X-ray crystallography, 1.5 angstroms
R:Leguin, O.; Albaret, C.; Bontems, F.; Spik, G.; Lallemand, J.Y.
submitted to the Brookhaven Protein Data Bank, April 1996
A:Reference number: A65709; PDB:1G10
A:Contents: annotation; conformation by (1)H-NMR, residues 1-125
R:Leguin, O.; Albaret, C.; Bontems, F.; Spik, G.; Lallemand, J.Y.
Biochemistry 35, 8870-8880, 1996
A>Title: Solution structure of bovine angiotensin by (1)H nuclear magnetic resonance spectroscopy.
A:Reference number: A58821; MUID:96280645; PMID:8688423
A:Contents: annotation; conformation by (1)H-NMR
R:Reisdorf, C.; Abert, D.; Bontems, F.; Lallemand, J.Y.; Decottignies, J.P.; Spik, G.
Eur. J. Biochem. 224, 811-822, 1994
A>Title: Proton resonance assignments and secondary structure of bovine angiotensin.
A:Reference number: S48212; MUID:95010071; PMID:7925406
A:Contents: annotation; conformation by (1)H-NMR
A:Function:
A:Description: hydrolyzes tRNA; induces vascularization of normal and malignant tissues
C:Superfamily: pancreatic ribonuclease
C:Keywords: angiogenesis; hydrolase; nucleic acid degradation
F:60-68/Region: receptor binding #status predicted
F:14,41,119/Active site: His, Lys, His #status predicted
F:27-82,40-93,58-108/Diulfide bonds: #status experimental

Query Match 21.7%; Score 125; DB 1; Length 125;
Best Local Similarity 33.0%; Pred. No. 1.6e-05;
Matches 32; Conservative 15; Mismatches 32; Indels 18; Gaps 5;

16 DVDGNILSTLNF--HCKDKNFTYRSREPVKAIKGIISKV-----VLITSEFYL 65
Db 24 DEYCNMMKMKRRLTRPCDKDRNFTFGNKNDIKALICE---DRNGQPYRGDLRIKSKSEFOI 79

66 SDC--NVTSR--PCRYKLKSTNFTFCVTCENQAPVHF 98
Db 80 TICGKGGSSRPCKRYGATSDSRVIVGCEGCLPVPHF 116

RESULT 8
NRCU
pancreatic ribonuclease (EC 3.1.27.5) - nutria (tentative sequence)
N:Alternate names: RNase 1; RNase A
C:Species: Myocastor coypus (nutria, coypu)
C>Date: 24-Apr-1984 #sequence_revision 30-Sep-1988 #text_change 31-Mar-2000
C:Accession: A00822
R:van den Berg, A.; van den Hende-Timmer, L.; Beintema, J.J.
Biochim. Biophys. Acta 453, 400-409, 1976
A>Title: Isolation, properties and primary structure of coypu and chinchilla pancreatic
A:Reference number: A90612; MUID:77065676; PMID:999896
A:Accession: A00822
A:Molecule type: protein

A:Residues: 1-128 <VAN>
C:Superfamily: pancreatic ribonuclease
C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F:12,41,119/Active site: His, Lys, His #status predicted
F:26-84,40-95,58-110,65-72/Diulfide bonds: #status predicted
F:34/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 21.3%; Score 123; DB 1; Length 128;
Best Local Similarity 29.1%; Pred. No. 2.6e-05;
Matches 34; Conservative 19; Mismatches 36; Indels 28; Gaps 7;

6 FOKKLU-----TNTSDVDCNNIL--STNLF--HCKDKNFTYRSREPVKAIKGIISKV 57
Db 8 FERQHMDSRGSPSTPNYCNEMKSRNMTQGRCKPVNTFVHPLADVQAVC----FOKQV 63

58 L-----TTSEFYLSDCNVTSRP----CKYKLKSTNFTFCVTCENQ--APVHF 98
Db 64 LCKNGQTNCGQSNMWHITDCRVTSNDPVNCSYRSTQSEKSIIVACEGNPVVPVHF 120

RESULT 9
NRMHK
pancreatic ribonuclease (EC 3.1.27.5) - minke whale
N:Alternate names: RNase 1; RNase A
C:Species: Balenoptera acutorostrata (minke whale, lesser rorqual)
C>Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 03-Jun-1994
C:Accession: A00818
R:Bommens, M.; Welling, G.W.; Beintema, J.J.
Biochem. J. 157, 317-323, 1976
A>Title: The amino acid sequence of pike whale (lesser rorqual) pancreatic ribonuclease.
A:Reference number: A00818; MUID:76377855; PMID:962870
A:Accession: A00818
A:Molecule type: protein
A:Residues: 1-124
C:Superfamily: pancreatic ribonuclease
C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F:12,41,119/Active site: His, Lys, His #status predicted
F:26-84,40-95,58-110,65-72/Diulfide bonds: #status predicted
F:76/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 21.1%; Score 122; DB 1; Length 124;
Best Local Similarity 27.7%; Pred. No. 3.2e-05;
Matches 33; Conservative 16; Mismatches 42; Indels 28; Gaps 6;

4 LTFQKHLTNRDND-----CNNILSTLNF--HCKDKNFTYRSREPVKAIKGIISKV 55
Db 6 MKFORHMDSGNSPNNPNYCNQMMMRKMTQGRCKPVNTFVHESLFDVKAVC---SQK 61

56 NVL-----TTSEFYLSDCNVTSRP----CKYKLKSTNFTFCVTCENQ--APVHF 98
Db 62 NVLCKNGRTNCTYESNSTWHITDCRVTSNDPVNCSYRSTQSEKSIIVACEGNPVVPVHF 120

RESULT 10
A35932
angiotensin precursor - mouse
N:Alternate names: angiotensin factor
N:Contains: ribonuclease (EC 3.1.27.-)
C:Species: Mus musculus (house mouse)
C>Date: 09-Nov-1990 #sequence_revision 09-Nov-1990 #text_change 18-Jun-1999
C:Accession: A35932
R:Bond, M.D.; Vallee, B.L.
Biochem. Biophys. Res. Commun. 171, 988-995, 1990
A>Title: Isolation and sequencing of mouse angiotensin DNA.
A:Reference number: A35932; MUID:91025023; PMID:2222458
A:Accession: A35932
A>Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-145 <BON>
A:Cross-references: GB:U022516; NID:g726325; PIDN:AAA91366.1; PID:g726326
C:Genetics:
A:introns: #status absent
C:Function:

A:Superfamily: hydrolyzes tRNA; induces vascularization of normal and malignant tissues
C:Description: pancreatic ribonuclease
C:Keywords: angiogenesis; hydrolase; nucleic acid degradation; pyroglutamic acid
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-145/Product: angiotensin #status predicted <MAT>
F:25/Modified site: pyrrolidone carboxylic acid (Gln) (1n mature form) #status predicted
F:37-64/137/Active site: His, Lys, His #status predicted
F:50-104, 63-115, 81-130/Disulfide bonds: #status predicted

Query Match	20.5%	Score 118.5	DB 1	Length 145
Best Local Similarity	35.5%	Pred No. 8.4e-05		
Matches 27	Conservative 11	Mismatches 31	Indels 7	Gaps 3

Db

```
OY      30 CKDKTKFIYSRPEPPVAIC--KGLIISKNV-LTTSELYSDENVT-----RPCKYKLKKKS   82  
          ||| :||| |  
        63 CKDVVTFIHGKNKNIKAICGANSGSPRENLNRMSKSPQVVTCHTGTGGSPRRPCGYRASAG  122
```

QY	83	TNTFCVTCENQAPVHF	98
		:	
Db	123	FRHVVIACENGLPVHF	138

RESULT 11

pancreatic ribonuclease (EC 3.1.27.5) - casiragua
C1:Species: Proechimys guairae (casiragua)
C1:date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 30-Sep-1993
C1:Accession: 000001

A. Beintema, J. J. ; Knol, G. ; Martena, B. Biochim. Biophys. Acta 705, 102-110, 1982

A. Title: The primary structures of pancreatic ribonucleases from African porcupine and

A:Accession: A00821
A:Molecule type: protein
A:Residues: 1-128 <BET>
A:Note: residues 67-78 were positioned primarily by homology with other ribonucleases
C:Superfamily: pancreatic ribonuclease
C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F:126-84,40-95,-58-110,65-72/Disulfide bonds: #status predicted
F:34/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match	20.3%	Score 117	DB 1	Length 128
Best Local Similarity	29.1%	Pred. No. 0.00011		
Matches 34	Conservative 19	Mismatches 36	Indels 28	Gaps 7

[illegible]

```

Oy      58  -----LTTSEFYLSDCVNTR-----PCKYKLKSKSTNTPCVCVCENQ--APVHF 98
          :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
Db      64  PCKNGQSNCEYSTSMNHITDCRLTNSKFPDCLYRTSQGEKSLIVACEGNPYVPVHF 120

```

RESULT 12

angiotensin - rabbit
CISpecies: Oryctolagus cuniculus (domestic rabbit)
CjDate: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
CjAccession: S2983j; B4825
RjBond, M.D.: Strydom, D.J., Vallee, B.L.
Biochim. Biophys. Acta 1162, 177-186, 1993
AjTitle: Characterization and sequencing of rabbit, pig and mouse angiotensins: discernm
AjReference number: S2983j; MUID:93192291; PMID:8448182

A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-125 <BON>

C:Superfamily: pancreatic ribonuclease
C:Keywords: pyroglutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match	20.1%;	Score 116;	DB 1;	Length 125;
Best Local Similarity	31.2%;	Pred. No. 0.00013;		
Matches 24;	Conservative 13;	Mismatches 32;	Indels 8;	Gaps 3

QY 30 CKDKNTFIYSRPEPKAICK---GIILASIKV-LTTSEYLSDCNVT-----RPCKKYLKK 81

DB 39 CKDKNTFIYHGNKGSIKDVCEIDKNGKPKYGIKFIASIKSSFQVTTCKHVGSGSPWPCRYRATS 98

```
QY      82 STNFCVTCENQAPVHF 98
          : ||| |||
Db      99 GSRNIVIACENGLPVHF 115
```

RESULT 13

pancreatic ribonuclease (EC 3.1.27.5) B - guinea pig (tentative sequence)
N/Alternate names: RNase IB
C/Species: *Cavia porcellus* (guinea pig)

C:Accession: A00836
R:van den Berg, A.; van den Hende-Timmer, L.; Hofsteenge, J.; Gaasstra, W.; Beintema, J.J.
Riv. J. Biochem. 75, 91-100, 1977

A:Reference number: A91247; MUID:77185023; PMID:862624
A:Accession: A00826
A:Molecule type: protein

A:Note: 64-Pro was also found
C:Superfamily: pancreatic ribonuclease
C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas

F,12,41,119/Active site: His, Lys, His #status predicted
F,21,34/Binding site: carboxylate (Asn) (covalent) #status experimental
F,26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted

Query Match	20.1%	Score	116;	DB	1;	length	128;
Best Local Similarity	27.5%	Pred. No.	0.00013;				
Matches	33;	Conservative	22;	Mismatches	35;	Indels	30;
						Gaps	7

Oy 4 LTPQKHL-----TNTRDVDCNNIL---STWLHCKDKDNTFYSRPEPKVAICKGIIAS 54
::: :::: : ||| :: |
Db 6 MKFQRQHMPPEGSPNSNSTY-CNVMMIRRNMTGRCRKPVTTFVESLADVOAVC----PQ 60

```

Oy 55 KNTL-----TTSEFYLSDCNVTSRP---CKYKLKSTNTTCVTCENQ--APVHF 98
    ||| : ||| ||| : : : ||| |||
Db 61 KNTLCIKNGQTNQYSYRMRITDCRVTTSSSKFPNCSYRMSQAQSKIIVACEGDPVYPVPHF 120

```

RESULT 14

pancreatic ribonuclease (EC 3.1.27.5) - *Chinchilla brevicaudata* (tentative sequence)
N:Alternate names: RNase 1; RNase A
C:Species: *Chinchilla brevicaudata*, *Chinchilla lanigera brevicaudata*
C>Date: 24-Apr-1994 #sequence_revision 30-Sep-1988 #text_change 31-Mar-2000
C:Accession: A00820
R:van den Berg, A.; van den Herde-Timmer, L.; Beintema, J.J.
Biochim. Biophys. Acta 453, 400-409, 1976
R:Title: Isolation, properties and primary structure of copu and *chinchilla* pancreatic

A:Accession: A00820
A:Molecule type: protein
A:Residues: 1-124 <VAN>

C:Superfamily: pancreatic ribonuclease
C:Substrate: glycylglycine; hydrolysis
C:Keywords: glycoprotein; nucleic acid digestion; pancreas
P:12,41,119/Active site: His, Lys, His #status predicted

Query Match 19.8%; Score 114; DB 1; Length 124;
F,34/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match	19.8%	Score	114	DB	1	Length	124
Best Local Similarity	26.1%	Pred. NO.	0.0002				
Matches	31	Conservative	20	Mismatches	40	Indels	28
				Gaps			6

[illegible]

RESULT 15

pancreatic ribonuclease (EC 3.1.27.5) - capybara
N:Alternate names: RNase 1, RNase A
C:Species: Hydrochaeris hydrochaeris (capybara, carpincho)
C:Date: 03-Aug-1984 #sequence_revision 03-Aug-1984 #text_change 29-Oct-1999
C:Accession: A00824
R:Reinrega, J.J.; Neuteboom, B.
J. Mol. Evol. 19, 145-152, 1983
A:Title: Origin of the duplicated ribonuclease gene in guinea-pig: comparison of the amino acid sequence with that of the pancreatic ribonuclease
A:Reference number: A92957; MUID:87036770; PMID:6571219
A:Accession: A00824
A:Molecule type: protein
A:Residues: 1-128 <BE1>
C:Superfamily: pancreatic ribonuclease
C:Keywords: hydrolase; nucleic acid digestion; pancreas
F:2,41,119/Active site: His, Lys, His #status predicted
F:26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted

Query Match	Score	DB	Length
19.64	113	1	128
Best Local Similarity	27.04	0	00026

Matches 31; Conservative 22; Mismatches 42; Indels 20; Gaps 6;

[illegible]

Search completed: January 22, 2004, 12:03:21
Job time : 12.6854 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 22, 2004, 12:01:20 ; Search time 6.23221 Seconds

(without alignments)
784.758 Million cell updates/sec

Title: US-09-622-613C-4

Perfect score: 577

Sequence: 1 QDMVLFQKHLTNTRVDN.....TFCVTCENQAVHFGVGHG 104

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	553	95.8	104	1	P22069 rana pipien
2	289	50.1	111	1	RNP_O_RANCA
3	282.5	49.0	111	1	P11916 rana catesb
4	266.5	46.2	111	1	P18839 rana japoni
5	146	25.3	119	1	P14626 rana catesb
6	130.5	22.6	145	1	P80287 iguana igua
7	130.5	22.6	145	1	Q64438 mus musculu
8	128	22.2	124	1	Q8wn66 cercopithec
9	125	21.7	148	1	P00680 galea muste
10	123	21.3	128	1	RNP_MYOCO
11	122	21.1	124	1	P00673 myocastor c
12	121.5	21.1	146	1	P00673 balaenopter
13	118.5	20.5	145	1	Q8wn63 macaca mlla
14	118.5	20.5	145	1	P21570 mus musculu
15	117	20.3	128	1	Q8wn66 papio hamad
16	116	20.1	125	1	RNP_PROGU
17	116	20.1	125	1	RNP_PROGU
18	114	19.8	124	1	P13347 oryctolagus
19	113	19.6	128	1	P00679 cavia porce
20	113	19.6	146	1	P00677 chinchilla
21	113	19.6	146	1	Q8wn67 hydrochoeru
22	112	19.4	147	1	Q8wn63 mlopithecus
23	112	19.4	147	1	Q35290 mus musculu
24	111	19.2	124	1	P03950 homo sapien
25	109.5	19.0	123	1	Q8wn68 pan troglod
26	109	18.9	124	1	P00672 hippopotamu
27	109	18.9	150	1	P31346 sus scrofa
28	109	18.9	150	1	P00671 bos taurus
29	108.5	18.8	146	1	Q8wn61 myoxus glis
30	108	18.7	128	1	P34096 homo sapien
31	108	18.7	128	1	P00674 equus cabal
32	108	18.7	146	1	P04060 hystrix cri
33	108	18.7	167	1	Q8wn62 saginus oe
					P39873 bos taurus

ALIGNMENTS

RESULT 1	ID	QNT0_RANPI	STANDARD;	PRT;	104 AA.
AC	P22069;				
DT	01-AUG-1991 (Rel. 19, Created)				
DT	01-FEB-1994 (Rel. 28, Last sequence update)				
DT	28-FEB-2003 (Rel. 41, Last annotation update)				
DE	P-30 protein (EC 3.1.27.-) (Onconase).				
OS	Rana pipiens (Northern leopard frog).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.				
OX	NCBI_TaxID=8404;				
RM	(1)				
RP	SEQUENCE.				
RC	TISSUE=Embryo;				
RA	MEDLINE=91093131; PubMed=1985896;				
RA	Ardelt W., Mikulski S.M., Shogen K.;				
RT	"Amino acid sequence of an anti-tumor protein from Rana pipiens				
RT	oocytes and early embryos. Homology to pancreatic ribonucleases.";				
RL	J. Biol. Chem. 266:245-251 (1991).				
RM	(2)				
RP	3D-STRUCTURE MODELING.				
RC	MEDLINE=9306156; PubMed=1438177;				
RA	Mosimann S.C., Johns K.L., Ardelt W., Mikulski S.M., Shogen K.;				
RA	James M.N.G.;				
RT	"Comparative molecular modeling and crystallization of P-30 protein:				
RT	a novel anticancer protein of Rana pipiens oocytes and early				
RL	embryos.";				
RL	Proteins 14:392-400 (1992).				
RM	(3)				
RP	X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).				
RC	MEDLINE=94166079; PubMed=8120892;				
RA	Mosimann S.C., Ardelt W., James M.N.G.;				
RT	"Refined 1.7 A X-ray crystallographic structure of P-30 protein, an				
RT	amphibian ribonuclease with anti-tumor activity.";				
RL	J. Mol. Biol. 236:1141-1153 (1994).				
CC	-1- FUNCTION: BASIC PROTEIN WITH ANTIPROLIFERATIVE/CYTOTOXIC ACTIVITY				
CC	AGAINST SEVERAL TUMOR CELL LINES IN VITRO. AS WELL AS ANTITUMOR				
CC	IN VIVO. IT EXHIBITS A RIBONUCLEASE-LIKE ACTIVITY AGAINST HIGH				
CC	MOLECULAR WEIGHT RIBOSOMAL RNA.				
CC	-1- DEVELOPMENTAL STAGE: EARLY EMBRYOS (UP TO FOUR BLASTOMERE STAGE).				
CC	-1- SIMILARITY: Belongs to the pancreatic ribonuclease family.				
DR	PDB; IONC; 31-JAN-94.				
DR	InterPro: IPR001427; RnaSeA.				
DR	Pfam: PF00074; rnaSeA; 1.				
DR	SMART; SM00092; RnaSe_Pc; 1.				
DR	PROSITE; PS00127; RnaSe_PANCREATIC; 1.				
KW	Hydrolase; Nuclease; Endonuclease; 3D-structure;				
KW	Pyrolydine carboxylic acid.				
FT	MOD_RES	1	1		
FT	ACT_SITE	10	10		
FT	ACT_SITE	31	31		
FT	ACT_SITE	97	97		
FT	DISULFID	19	68		
FT	DISULFID	30	75		

FT DISULFID 48 90
 FT DISULFID 87 104
 FT HELIX 3 10
 FT STRAND 11 12
 FT HELIX 19 22
 FT TURN 23 24
 FT TURN 26 30
 FT STRAND 33 38
 FT HELIX 41 45
 FT HELIX 46 48
 FT TURN 49 50
 FT STRAND 55 58
 FT STRAND 63 70
 FT TURN 74 75
 FT STRAND 77 84
 FT STRAND 86 91
 FT TURN 92 93
 FT STRAND 94 101
 SQ SEQUENCE 104 AA; 11845 MW; 22A753C2F9E566B4 CRC64;

Query Match 95.8%; Score 553; DB 1; Length 104;
 Best Local Similarity 95.2%; Pred. No. 5, 1e-52;
 Matches 99; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 ODMLTFOKKHLLTNRDVCNNILSTNLFHCKDKNTFIYSRPPVKAICKGIASKVLT 60
 DB 1 ODMLTFOKKHLLTNRDVCNNILSTNLFHCKDKNTFIYSRPPVKAICKGIASKVLT 60
 OY 61 SEFYLSDCNVTSPCKYKLSKSTNTFCVTCENQAPVHFGVGHG 104
 DB 61 SEFYLSDCNVTSPCKYKLSKSTNTFCVTCENQAPVHFGVGHG 104

RESULT 2
 ID RNPO_RANCA STANDARD; PRT; 111 AA.
 AC P11916;

DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ribonuclease, oocytes (EC 3.1.27.-) (RC-RNase) (Sialic acid-binding lectin) (SBL-C).
 DE Rana catesbeiana (Bull. frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
 OX NCBI_TaxID=8400;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=EGG;
 RX MEDLINE=87296649; PubMed=3304421;
 RA Takeyama G., Takio K., Kuwada M., Nitta K., Sakakibara F., Kawachi H., Takeyama G., Hakomori S.,
 RT "Am. no acid sequence of sialic acid binding lectin from frog (Rana catesbeiana) eggs.";
 RL Biochemistry 26:2189-2194 (1987).
 RN [2]
 RP CHARACTERIZATION, AND SEQUENCE OF 59-79.
 RX MEDLINE=92220613; PubMed=1373237;
 RA Liao Y.-D.;
 RT "A pyrimidine-guanine sequence-specific ribonuclease from Rana catesbeiana (bullfrog) oocytes.";
 RL Nucleic Acids Res. 20:1371-1377 (1992).
 RN [3]
 RP CHARACTERIZATION.
 RC TISSUE=EGG;
 RX MEDLINE=93192604; PubMed=8448385;
 RA Nitta K., Oyama F., Oyama R., Sekiguchi K., Kawachi H., Takeyama G., Hakomori S., Takio K.;
 RT "Ribonuclease activity of sialic acid-binding lectin from Rana catesbeiana eggs.";
 RL Glycobiology 3:37-45 (1993).
 RN [4]
 RP STRUCTURE BY NMR.

RX MEDLINE=98437383; PubMed=9761686;
 RA Chang C.-F., Chen C., Chen Y.-C., Hom K., Huang R.-F., Huang T.H.;
 RT "The solution structure of a cytotoxic ribonuclease from the oocytes of Rana catesbeiana (bullfrog).";
 RL J. Mol. Biol. 283:231-244 (1998).

CC -1- FUNCTION: Preferentially cleaves single-stranded RNA at pyrimidine residues with a 3' flanking guanine. Hydrolyzes poly(U) and poly(C) as substrates, and prefers the former. The S-lectins in frog eggs may be involved in the fertilization and development of the frog embryo. This lectin agglutinates various animal cells, including normal lymphocytes, erythrocytes, and fibroblasts of animal and human origin.

CC -1- SUBUNIT: Monomer.
 CC -1- SUBCELLULAR LOCATION: Secreted.

DR PIR: A27121; A27121.
 DR PDB: 1BC4; 28-OCT-98.
 DR PDB: 1M07; 21-JAN-03.
 DR InterPro: IPR001427; RNaseA.
 DR Pfam: PF00074; RNaseA; 1.
 DR ProDom: PD000535; RNaseA; 1.
 DR SMART: SM00092; RNase_Pc; 1.
 DR PROSITE: PS00127; RNASE_PANCREATIC; 1.

KW Hydrolase; Nuclease; Endonuclease; Sialic acid; Lectin; 3D-structure; Pyroliidone carboxylic acid. PYROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 1 1
 FT ACT_SITE 10 10
 FT ACT_SITE 35 35
 FT ACT_SITE 103 103
 FT DISULFID 19 71
 FT DISULFID 34 81
 FT DISULFID 52 96
 FT DISULFID 93 110
 FT HELIX 3 10
 FT HELIX 19 23
 FT TURN 26 27
 FT STRAND 37 41
 FT HELIX 45 51
 FT TURN 52 52
 FT STRAND 57 62
 FT STRAND 68 73
 FT STRAND 83 88
 FT STRAND 92 97
 FT TURN 98 99
 FT STRAND 100 107
 SQ SEQUENCE 111 AA; 12464 MW; 0BC9E5F55729ECF4 CRC64;

Query Match 50.1%; Score 289; DB 1; Length 111;
 Best Local Similarity 48.6%; Pred. No. 5, 4e-24;
 Matches 54; Conservative 17; Mismatches 32; Indels 8; Gaps 3;

OY 1 ODMLTFOKKHLLTNRDVCNNILSTNLFHCKDKNTFIYSRPPVKAICKGIASKV 56
 DB 1 ODMATFOKKHLLTNRDVCNNILSTNLFHCKDKNTFIYSRPPVKAICKGIASKV 59
 OY 57 VLTSEFYLSDC--NVTSPCKYKLSKSTNTFCVTCENQAPVHFGVGHG 104
 DB 60 VLTSPFOLNCTRTSPCKYKLSKSTNTFCVTCENQAPVHFGVGHG 110

RESULT 3
 ID LEC3_RANJA STANDARD; PRT; 111 AA.
 AC P18839;

DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Sialic acid-binding lectin (EC 3.1.27.-).
 OS Rana japonica (Japanese Reddish frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
 OX NCBI_TaxID=8402;
 RN [1]

RP SEQUENCE, AND DISULFIDE BONDS.
RC TISSUE=Egg;
RX MEDLINE=91035319; PubMed=2229005;
RA Kamiya Y., Oyama F., Oyama R., Sakakibara F., Nitta K., Kawachi H.,
RT Takayanagi Y., Tltani K.;
RT "Amino acid sequence of a lectin from Japanese frog (Rana japonica)
eggs.";
RL J. Biochem. 108:139-143(1990).
CC -1- FUNCTION: THE S-LECTINS IN FROG EGGS MAY BE INVOLVED IN THE
CC FERTILIZATION AND DEVELOPMENT OF THE FROG EMBRYO. THIS LECTIN
CC PREFERENTIALLY AGGLUTININATE A LARGE VARIETY OF TUMOR CELLS, BUT IT
CC DOES NOT AGGLUTINATE NON-TRANSFORMED CELLS AND ERYTHROCYTES.
CC -1- SUBUNIT: Monomer.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the pancreatic ribonuclease family.
DR PIR, JX0120, JX0120.
DR HSSP, P11916, 1BC4.
DR InterPro, IPR001427; RNaseA.
DR Pfam, PF00074; RNaseA; 1.
DR ProDom, PD000535; RNaseA; 1.
DR SMART, SM00092; RNase_Pc; 1.
DR PROSITE, PS00127; RNASE_PANCREATIC; 1.
KM Hydroxylase; Nuclease; Endonuclease; Sialic acid; Lectin;
KM Pyrolydione carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT ACT_SITE 10 10 BY SIMILARITY.
FT ACT_SITE 35 35 BY SIMILARITY.
FT ACT_SITE 104 104 BY SIMILARITY.
FT DISULFID 19 72 BY SIMILARITY.
FT DISULFID 34 82
FT DISULFID 52 97
FT DISULFID 94 111
SQ SEQUENCE 111 AA; 12326 MW; FDEBDDF3834ED679 CRC64;

Query Match 49.0%; Score 282.5; DB 1; Length 111;
Best Local Similarity 44.1%; Pred. No. 2.7e-23;
Matches 49; Conservative 20; Mismatches 35; Indels 7; Gaps 2;

Qy 1 QDMLTFQKHLNTRDVCNNILSTNLF---HCKDKNFTIYSRPEPVAKICKGIASRN 56
Db 1 QWMAFKFKHIRSTSIDCNTIMDKAIYIVGGCKCKERNFTIISATTVAAICSGASTWKN 60
111
57 VLTSEFYLSDC--NVTSRPCKYKLLKKSNTFCVTGCENQAPVHFVGCHC 104
61 VLSTTRFQNLTCIRDSATAPRCPVNSRTETNIVICVCKENRLEPVHFAGIGRC 111

RESULT 4
ID RNPL_RANCA STANDARD; PRT; 111 AA.
AC P14626;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ribonuclease, liver (EC 3.1.27.5).
OS Rana catesbeiana (Bull) frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
OX NCBI_Taxid=8400;
RN [1]
RP SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=90130374; PubMed=2613682;
RA Nitta R., Katayama N., Okabe Y., Iwama M., Watanabe H., Abe Y.,
RT Okazaki T., Ohgi K., Irie M.;
RT "Primary structure of a ribonuclease from bullfrog (Rana catesbeiana)
liver.";
RL J. Biochem. 106:729-735(1989).
CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
CC phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
CC with 2',3'-cyclic phosphate intermediates.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the pancreatic ribonuclease family.

DR PIR, JX0085, JX0085.
DR HSSP, P11916, 1BC4.
DR InterPro, IPR001427; RNaseA.
DR Pfam, PF00074; RNaseA; 1.
DR ProDom, PD000535; RNaseA; 1.
DR SMART, SM00092; RNase_Pc; 1.
DR PROSITE, PS00127; RNASE_PANCREATIC; 1.
KM Hydroxylase; Nuclease; Endonuclease; Pyrolydione carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT ACT_SITE 10 10 BY SIMILARITY.
FT ACT_SITE 35 35 BY SIMILARITY.
FT ACT_SITE 104 104 BY SIMILARITY.
FT DISULFID 19 72 BY SIMILARITY.
FT DISULFID 34 82 BY SIMILARITY.
FT DISULFID 52 97 BY SIMILARITY.
FT DISULFID 94 111 PROBABLE.
SQ SEQUENCE 111 AA; 12461 MW; D64BA72456C10788 CRC64;

Query Match 46.2%; Score 266.5; DB 1; Length 111;
Best Local Similarity 42.3%; Pred. No. 1.3e-21;
Matches 47; Conservative 20; Mismatches 37; Indels 7; Gaps 2;

Qy 1 QDMLTFQKHLNTRDVCNNILSTNLF---HCKDKNFTIYSRPEPVAKICKGIASRN 56
Db 1 QWMAFKFKHIRSTSIDCNTIMDKAIYIVGGCKCKERNFTIISBDNVAKICGVSPDK 60
111
57 VLTSEFYLSDC--NVTSRPCKYKLLKKSNTFCVTGCENQAPVHFVGCHC 104
61 ELSTSFQNLTCIRDSITPRCPVNSPDNNKICVCKEQKQVHFVGIGKC 111

RESULT 5
ID RNPL_IGUIG STANDARD; PRT; 119 AA.
AC P80287;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ribonuclease pancreatic (EC 3.1.27.5) (RNase A).
OS Iguana iguana (Common Iguana).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodactylia; Squamata; Iguania; Iguanidae; Iguaninae; Iguana.
OX NCBI_Taxid=8517;
RN [1]
RP SEQUENCE.
RC TISSUE=Pancreas;
RX MEDLINE=94139745; PubMed=8307028;
RA Zhao W., Beintema J.J., Hofsteenge J.;
RT "The amino acid sequence of iguana (Iguana iguana) pancreatic
ribonuclease.";
RL Eur. J. Biochem. 219:641-646(1994).
CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
CC phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
CC with 2',3'-cyclic phosphate intermediates.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Pancreas.
CC -1- SIMILARITY: Belongs to the pancreatic ribonuclease family.
DR PIR, S41111, S41111.
DR HSSP, P00656, 1LSQ.
DR InterPro, IPR001427; RNaseA.
DR Pfam, PF00074; RNaseA; 1.
DR PRINTS, PR00794; RIBONUCLEASE.
DR ProDom, PD000535; RNaseA; 1.
DR SMART, SM00092; RNase_Pc; 1.
DR PROSITE, PS00127; RNASE_PANCREATIC; 1.
KM Hydroxylase; Nuclease; Endonuclease; Pyrolydione carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT ACT_SITE 10 10 BY SIMILARITY.
FT ACT_SITE 39 91 BY SIMILARITY.
FT DISULFID 57 106 BY SIMILARITY.
FT ACT_SITE 10 10 BY SIMILARITY.
FT ACT_SITE 40 40 BY SIMILARITY.
FT ACT_SITE 113 113 BY SIMILARITY.


```

Db 53 TWRRLHLS-----CKDINTFIHGRHHIKKICDGENGPYGENLRISK 97
OY 61 SEFYLSDDCVNTS-----RCKYKLKSKSTNTFCVTCEQAVH 97
Db 98 SPFOVTCNLGRGSPRPPCYATRGSRNIIVGCEGLPVA 138

RESULT 8
RNP_GALMU
ID RNP_GALMU STANDARD; PRT; 124 AA.
AC P00680;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).
GN RNASE1 OR RN51.
OS Galea musceloides (Cuis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriocognathi; Caviidae; Galea.
OX NCBI_TaxId=10146;
RN [1]
RP SEQUENCE.
RX MEDLINE=87036770; PubMed=6571219;
RA Beintema J.J., Neuteboom B.;
RT "Origin of the duplicated ribonuclease gene in guinea-pig: comparison
RT of the amino acid sequences with those of two close relatives:
RT capybara and cuia ribonuclease.";
RL J. Mol. Evol. 19:145-152(1983).
CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
CC phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
CC with 2',3'-cyclic phosphate intermediates.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Pancreas.
CC -1- SIMILARITY: Belongs to the pancreatic ribonuclease family.
DR HSP; A00827; NEUT.
DR HSP; P00656; ISRN.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; RNaseA; 1.
DR PRINTS: PRO0794; RIBONUCLEASE.
DR ProDom: PD000535; RNaseA; 1.
DR SMART: SMO0092; RNase_Pc; 1.
DR PROSITE: PS00127; RNASE_PANCREATIC; 1.
KW Hydrolyase; Nuclease; Endonuclease.
FT DISULFID 26 84 BY SIMILARITY.
FT DISULFID 40 95 BY SIMILARITY.
FT DISULFID 58 110 BY SIMILARITY.
FT DISULFID 65 72 BY SIMILARITY.
FT ACT_SITE 12 12 BY SIMILARITY.
FT ACT_SITE 41 41 BY SIMILARITY.
FT ACT_SITE 119 119 BY SIMILARITY.
FT VARIANT 1 1 MISSING (IN 1/3 OF THE MOLECULES).
SQ SEQUENCE 124 AA; 13870 MW; 609C7E251A7BBA25 CRC64;

Query Match 22.2%; Score 128; DB 1; Length 124;
Best Local Similarity 29.8%; Pred. No. 7.4e-07;
Matches 36; Conservative 19; Mismatches 34; Indels 32; Gaps 7;
OY 4 LTFQKHL-----TNTRDVDCNNIL-----STNLFHCKDKTFTYSRREPKAICKGIIA 53
Db 6 MKPGRQMDSDGHDITN--YCEBEMWRNSMTGRCRCPVTFVHEPLEAVQAVC-----S 59
OY 54 SKNV-----LTTSEFYLSDDCVNTSRP-----CKYKLKSKSTNTFCVTCE--QAPVH 97
Db 60 QKVPCKNGQGTNCYQSHSSMKRITDCRVTSSESKYPNCGRPMQAQKSIIVACEGTPSPVPH 119
OY 98 F 98
Db 120 F 120

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ID ANGI BOVIN STANDARD; PRT; 148 AA.
AC P10152; O9GKPP9;
DT 01-MAR-1989 (Rel. 10, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Angiogenin-1 precursor (EC 3.1.27.-).
GN ANGI OR ANG.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxId=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Chang S.-I.;
RT "Cloning, sequencing, and expression of bovine angiogenin.";
RL Submitted (MAR-1999) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE OF 24-148.
RC TISSUE=Milk;
RX MEDLINE=89065101; PubMed=3197838;
RA Maes P., Damart D., Rommens C., Montreuil J., Spik G., Tartar A.;
RT "The complete amino acid sequence of bovine milk angiogenin.";
RL FEBS Lett. 241:41-45(1988).
RN [3]
RP SEQUENCE OF 24-148.
RC TISSUE=Plasma;
RX MEDLINE=89375344; PubMed=2775757;
RA Bond M.D., Strydom D.J.;
RT "Amino acid sequence of bovine angiogenin.";
RL Biochemistry 28:6110-6113(1989).
RN [4]
RP CHARACTERIZATION, AND SEQUENCE OF 25-55.
RC TISSUE=Plasma;
RX MEDLINE=89118214; PubMed=3064806;
RA Bond M.D., Vallée B.L.;
RT "Isolation of bovine angiogenin using a placental ribonuclease
RT inhibitor binding assay.";
RL Biochemistry 27:6282-6287(1988).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS).
RX MEDLINE=95224057; PubMed=7708754;
RA Acharya K.R., Shapiro R., Riordan J.F., Vallée B.L.;
RT "Crystal structure of bovine angiogenin at 1.5-A resolution.";
RL Proc. Natl. Acad. Sci. U.S.A. 92:2949-2953(1995).
RN [6]
RP STRUCTURE BY NMR.
RX MEDLINE=96280645; PubMed=8688423;
RA Leguin O., Albaret C., Bontems F., Spik G., Lallemand J.-Y.;
RT "Solution structure of bovine angiogenin by 1H nuclear magnetic
RT resonance spectroscopy.";
RL Biochemistry 35:8870-8880(1996).
RN [7]
RP FUNCTION: MAY FUNCTION AS A TRNA-SPECIFIC RIBONUCLEASE THAT BINDS
RP TO ACTIN ON THE SURFACE OF ENDOTHELIAL CELLS; ONCE BOUND,
RP ANGIOGENIN IS ENDOCYTOSED AND TRANSLOCATED TO THE NUCLEUS, THEREBY
RP PROMOTING THE ENDOTHELIAL INVASIVENESS NECESSARY FOR BLOOD AND
RP LYMPHATIC TISSUES. ABOLISHES PROTEIN SYNTHESIS BY SPECIFICALLY
RP HYDROLYZING CELLULAR TRNAS. BINDS TIGHTLY TO PLACENTAL
RP RIBONUCLEASE INHIBITOR AND HAS VERY LOW RIBONUCLEASE ACTIVITY.
RN [8]
RP SUBCELLULAR LOCATION: Secreted.
RN [9]
RP TISSUE SPECIFICITY: SERUM, AND MILK.
RN [10]
RP SIMILARITY: Belongs to the pancreatic ribonuclease family.
RN [11]
RP This SWISS-PROT entry is copyright. It is produced through a collaboration
RN between the Swiss Institute of Bioinformatics and the EMBL outstation -
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RN or send an email to license@isb-ebi.ch).

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Db 6 MKFGRHDSGNSPGNNPNYCNQMMRRKMGORCKPVTNFVHESLEDYKAVC----SQK 61
 QY 56 NVL-----TSEFLSDCNVTSR-----CKYKLSKSTNFTCYTENQ--APVAF 98
 Db 62 NVLCNGRGTNCYESNSTHMTDRCROTGSSEKYPNCAYKTSQKSKHIVACEGNPYVPVHF 120

RESULT 12

ANGI_MOUSE STANDARD; PRT; 146 AA.
 ID ANGI_MOUSE
 AC Q8WNG3;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Angiogenin precursor (EC 3.1.27.-) (Ribonuclease 5) (RNase 5).
 GN ANG OR RNASES.
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Macaca.
 OX NCBI_TaxID=9544;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21918422; PubMed=11919285;
 RA Zhang J., Rosenberg H.F.;
 RT "Diversifying selection of the tumor-growth promoter angiogenin in primate evolution.";
 RL Mol. Biol. Evol. 19:438-445(2002).
 CC - FUNCTION: MAY FUNCTION AS A TRNA-SPECIFIC RIBONUCLEASE THAT BINDS TO ACTIN ON THE SURFACE OF ENDOTHELIAL CELLS; ONCE BOUND, ANGIOENIN IS ENDOCYTOSED AND TRANSLOCATED TO THE NUCLEUS, THEREBY PROMOTING THE ENDOTHELIAL INVASIVENESS NECESSARY FOR BLOOD VESSEL FORMATION. ANGIOENIN INDUCES VASCULARIZATION OF NORMAL AND MALIGNANT TISSUES. ABOLISHES PROTEIN SYNTHESIS BY SPECIFICALLY HYDROLYZING CELLULAR TRNAS (By similarity).
 CC - SUBCELLULAR LOCATION: Secreted.
 CC - SIMILARITY: Belongs to the pancreatic ribonuclease family.

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 CC -----
 CC EMBL, AF441667; AAL61649.1; -.
 DR InterPro: IPR001427; RNaseA.
 DR Pfam: PF00074; RNaseA; 1.
 DR ProDom: PD000535; RNaseA; 1.
 DR SMART: SMO0092; RNase_Pc; 1.
 DR PROSITE: PS00127; RNASE_PANCREATIC; 1.
 KM Hydroxylase; Nuclease; Endonuclease; Angiogenesis;
 KW Protein synthesis inhibitor; Signal; Pyrolydine carboxylic acid.
 FT SIGNAL 1 24
 FT CHAIN 25 146
 FT MOD_RES 25 25
 FT ACT_SITE 37 37
 FT ACT_SITE 64 64
 FT ACT_SITE 138 138
 FT DISULFID 50 105
 FT DISULFID 63 116
 FT DISULFID 81 131
 SEQUENCE 146 AA; 16301 MW; E39A89215DB2A244 CRC64;

Query Match 21.1%; Score 121.5; DB 1; Length 146;
 Best Local Similarity 28.7%; Pred. No. 4.3e-06;
 Matches 29; Conservative 17; Mismatches 32; Indels 23; Gaps 4;

OY 5 TFOKKHLNTNDVCCNLTSLNLFHCKDKNTFIYRPREPVAKC---KGIASKV-LTT 60
 Db 53 TMRRLHTSP-----CKDINTFVGNRHHTALICDENGSPYGNLRIST 97

QY 61 SEFLSDCNVTS-----RCKYKLSKSTNFTCYTENQAPVH 97
 Db 98 SFFQVTTCKLRGSSPRPCQYRATGRSNRIIVGCEGLPVH 138

RESULT 13

ANGI_MOUSE STANDARD; PRT; 145 AA.
 ID ANGI_MOUSE
 AC P21570;
 DT 01-MAY-1991 (Rel. 18, Created)
 DT 01-MAY-1991 (Rel. 18, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Angiogenin precursor (EC 3.1.27.-) (Ribonuclease 5) (RNase 5).
 GN ANG.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91025023; PubMed=2222458;
 RA Bond M.D., Vallee B.L.;
 RT "Isolation and sequencing of mouse angiogenin DNA.";
 RL Biochem. Biophys. Res. Commun. 171:988-995(1990).
 RN (2)
 RP PARTIAL SEQUENCE.
 RC TISSUE=serum;
 RX MEDLINE=93192291; PubMed=8448182;
 RA Bond M.D., Struydom D.J., Vallee B.L.;
 RT "Characterization and sequencing of rabbit, pig and mouse angiogenins: discernment of functionally important residues and regions.";
 RL Biochim. Biophys. Acta 1162:177-186(1993).

CC - FUNCTION: MAY FUNCTION AS A TRNA-SPECIFIC RIBONUCLEASE THAT BINDS TO ACTIN ON THE SURFACE OF ENDOTHELIAL CELLS; ONCE BOUND, ANGIOENIN IS ENDOCYTOSED AND TRANSLOCATED TO THE NUCLEUS, THEREBY PROMOTING THE ENDOTHELIAL INVASIVENESS NECESSARY FOR BLOOD VESSEL FORMATION. ANGIOENIN INDUCES VASCULARIZATION OF NORMAL AND MALIGNANT TISSUES. ABOLISHES PROTEIN SYNTHESIS BY SPECIFICALLY HYDROLYZING CELLULAR TRNAS.
 CC - SUBCELLULAR LOCATION: Secreted.
 CC - SIMILARITY: Belongs to the pancreatic ribonuclease family.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation at the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL, U22516; AAA91366.1; -.
 DR HSR; A35932; A35932.
 DR PIR; P03950; 1A4Y.
 DR MGD; MGI:88023; Ang.
 DR InterPro: IPR001427; RNaseA.
 DR Pfam; PF00074; RNaseA; 1.
 DR PRINTS; PR00794; RIBONUCLEASE.
 DR ProDom: PD000535; RNaseA; 1.
 DR SMART: SMO0092; RNase_Pc; 1.
 DR PROSITE: PS00127; RNASE_PANCREATIC; 1.
 KM Hydroxylase; Nuclease; Endonuclease; Angiogenesis;
 KW Protein synthesis inhibitor; Signal; Pyrolydine carboxylic acid.
 FT SIGNAL 1 24
 FT CHAIN 25 145
 FT MOD_RES 25 25
 FT ACT_SITE 37 37
 FT ACT_SITE 64 64
 FT ACT_SITE 137 137
 FT DISULFID 50 104
 FT DISULFID 63 115

Query Match 21.1%; Score 121.5; DB 1; Length 146;
 Best Local Similarity 28.7%; Pred. No. 4.3e-06;
 Matches 29; Conservative 17; Mismatches 32; Indels 23; Gaps 4;

Search completed: January 22, 2004, 12:02:08
Job time : 6.23221 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 22, 2004, 12:01:21 (Search time 25.7079 Seconds
(without alignments)
1043.940 Million cell updates/sec

Title: US-09-622-613C-4
Perfect score: 577
Sequence: 1 QDWLTFOCKKHLTNRDVDCN.....TFCVTCENQAPVHPVGVGHC 104

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_23:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriophage:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	575	99.7	127	13	Q918V8
2	553	95.8	127	13	Q8UVX5
3	401.5	69.6	129	13	Q9DFY6
4	383	66.4	128	13	Q9DFY7
5	308	53.4	128	13	Q9DFY7
6	306	53.0	128	13	Q9DFY5
7	295	51.1	133	13	Q9DSMO
8	289	50.1	133	13	Q9PWR7
9	283	49.0	133	13	Q9PWR7
10	282	48.9	132	13	Q9PWR7
11	279	48.4	133	13	Q9PWR7
12	277	48.0	132	13	Q9PWR7
13	272.5	47.2	132	13	Q9PWR7
14	156.5	27.1	169	13	Q9W738
15	128	22.2	157	11	Q9JKI9
16	127	22.0	157	11	Q9JKJ3

17	126	21.8	152	11	Q9JKI5	Q9JKI5 mus saxicol
18	126	21.8	157	11	Q9JKI4	Q9JKI4 meriones un
19	123.5	21.4	153	11	Q9JKI7	Q9JKI7 mus saxicol
20	123	21.3	157	11	Q9JKI1	Q9JKI1 meriones un
21	122	21.1	157	11	Q9JKI2	Q9JKI2 meriones un
22	120	20.8	154	11	Q9JKI8	Q9JKI8 mus saxicol
23	117.5	20.4	155	11	Q9JKI9	Q9JKI9 mus pahari
24	116.5	20.2	155	11	Q9JKI3	Q9JKI3 mus saxicol
25	114.5	19.8	155	11	Q9JKI8	Q9JKI8 mus pahari
26	113.5	19.7	155	11	Q9JKI6	Q9JKI6 mus gaxicol
27	113.5	19.7	155	11	Q9JKI6	Q9JKI6 mus gaxicol
28	112.5	19.5	155	11	Q9JKI2	Q9JKI2 mus saxicol
29	112.5	19.5	155	11	Q9JKI4	Q9JKI4 mus saxicol
30	112.5	19.5	155	11	Q9JKI4	Q9JKI4 mus saxicol
31	111.5	19.3	170	6	Q9BECL	Q9BECL tragulus ja
32	111	19.2	156	11	Q9JKG6	Q9JKG6 mus caroli
33	111	19.2	156	11	Q9JKG7	Q9JKG7 mus caroli
34	110.5	19.2	119	6	Q9TSO6	Q9TSO6 cercopithec
35	110.5	19.2	119	6	Q9TVJ2	Q9TVJ2 gorilla gor
36	110.5	19.2	147	6	Q9HZ00	Q9HZ00 pan troglod
37	110.5	19.2	155	11	Q9RI34	Q9RI34 ratius norv
38	110.5	19.2	155	11	Q9RI25	Q9RI25 mus musculu
39	110	19.1	156	11	Q9VHS0	Q9VHS0 mus musculu
40	110	19.1	156	11	Q9JKG7	Q9JKG7 mus caroli
41	109.5	19.0	119	6	Q9TVJ0	Q9TVJ0 saginus oe
42	109	18.9	124	6	Q9TSF2	Q9TSF2 bos taurus
43	109	18.9	156	11	Q9JKH4	Q9JKH4 mus caroli
44	109	18.9	156	11	Q9JKG9	Q9JKG9 mus caroli
45	109	18.9	156	11	Q9JKH5	Q9JKH5 mus caroli

ALIGNMENTS

RESULT 1
Q918V8 PRELIMINARY; PRT: 127 AA.

NC Q918V8: 01-OCT-2000 (TREMBL) 15, Created)
DT 01-OCT-2000 (TREMBL) 15, Last sequence update)
DT 01-MAR-2003 (TREMBL) 23, Last annotation update)
DE Onconase variant rap1 precursor.
OS Rana pipiens (Northern leopard frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CX Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.
NCBI_TaxID=8404;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=20330357; PubMed=10871370;
RA Chen S.-L., Le S.-Y., Newton D.L., Maizel J.V., Jr., Rybak S.M.,
RT "A gender-specific mRNA encoding a cytotoxic ribonuclease contains a
RT 3' UTR of unusual length and structure."
RL Nucleic Acids Res. 28:2375-2382(2000).
DR EMBL: AF165133; AAF76935.1; --
DR HSSP: P23069; 10NC.
DR InterPro: IPR001427; RNAseA.
DR Pfam: PF00074; RNAseA.1.
DR ProDom: PD000535; RNAseA.1.
DR SMART: SM00092; RNAse_Pc.1.
DR PROSITE: PS00127; RNAse_PANCREATIC.1.
KW Signal.
FT SIGNAL.
SQ SEQUENCE 127 AA; 14491 MW; B8511DC5407AB69B CRC64;

Query Match 99.7%; Score 575; DB 13; Length 127;
Best Local Similarity 99.0%; Pred. No. 4.5e-57;
Matches 103; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QDWLTFOCKKHLTNRDVDCNIIISTLFFCKDKKNTTYSRPEPVKAIKGIISKVLT 60
DB 24 QDWLTFOCKKHLTNRDVDCNIIISTLFFCKDKKNTTYSRPEPVKAIKGIISKVLT 83

```
OY 61 SEFYSDCNVTSRPRCKYKLTSTNTFCVTCENQAPVHFVGVGHC 104
DB 84 SEFYSDCNVTSRPRCKYKLTSTNTFCVTCENQAPVHFVGVGHC 127

RESULT 2
ID Q8UVX5 PRELIMINARY; PRT; 127 AA.
AC Q8UVX5;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Onconase precursor.
GN RPR.
OS Rana pipiens (Northern leopard frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
OX NCB1_Taxid=8404;
RN [1]
RP SEQUENCE FROM N.A.
RA Liao Y.-D., Wang S.-C.;
RT "Rana pipiens onconase genomic DNA."
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF332139; AAL54383.1; -
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; RNaseA; 1.
DR ProDom: PD000535; RNaseA; 1.
DR SMART: SM00092; RNase_Pc; 1.
DR PROSITE: PS00127; RNase_PANCREATIC; 1.
KW Signal.
FT SIGNAL.
SQ SEQUENCE 127 AA; 14469 MW; 953F90D351CFEEF3 CRC64;

Query Match
Best Local Similarity 95.8%; Score 553; DB 13; Length 127;
Matches 99; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 ODMLTFOKKHLTNRDVCNNILSTNLFPHCKDKNTFYISRPPEVPAICGIIASKNVLT 60
DB 24 QDMATFQKKHLTDVDDCNLMPTSLPDCCKDKNTFYISLGPVYALCRGVIFSAVDLSN 83

OY 61 SEFYSDCNVTSRPRCKYKLTSTNTFCVTCENQAPVHFVGVGHC 104
DB 84 SEFYSDCNVTSRPRCKYKLTSTNTFCVTCENQAPVHFVGVGHC 127

RESULT 3
ID Q9DFY6 PRELIMINARY; PRT; 129 AA.
AC Q9DFY6;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE RC-RNase4 ribonuclease precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
OX NCB1_Taxid=8400;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=20512555; PubMed=11058105;
RA Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.;
RT "Purification and cloning of cytotoxic ribonucleases from Rana
RT catesbeiana (bullfrog)."
RL Nucleic Acids Res. 28:4097-4104 (2000).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RA Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF242555; AAG31441.2; -.
DR HSSP: P22069; IONC.
DR HSSP: P22069; IONC.
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DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; RNaseA; 1.
DR ProDom: PD000535; RNaseA; 1.
DR PROSITE: PS00127; RNase_PANCREATIC; 1.
KW Signal.
FT SIGNAL.
FT CHAIN 24 129
SQ SEQUENCE 129 AA; 14724 MW; 826A62802B10ABDA CRC64;

Query Match
Best Local Similarity 69.6%; Score 401.5; DB 13; Length 129;
Matches 70; Conservative 17; Mismatches 17; Indels 1; Gaps 1;

OY 1 ODMLTFOKKHLTNRDVCNNILSTNLFPHCKDKNTFYISRPPEVPAICGIIASKNVLT 60
DB 24 QDMATFQKKHLTDVDDCNLMPTSLPDCCKDKNTFYISLGPVYALCRGVIFSAVDLSN 83

OY 61 SEFYSDCNVTSRPRCKYKLTSTNTFCVTCENQAPVHFVGVGHC 104
DB 84 SEFYSDCNVTSRPRCKYKLTSTNTFCVTCENQAPVHFVGVGHC 127

RESULT 4
ID Q9DFY8 PRELIMINARY; PRT; 128 AA.
AC Q9DFY8;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE RC-RNase2 ribonuclease precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
OX NCB1_Taxid=8400;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=20512555; PubMed=11058105;
RA Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.;
RT "Purification and cloning of cytotoxic ribonucleases from Rana
RT catesbeiana (bullfrog)."
RL Nucleic Acids Res. 28:4097-4104 (2000).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RA Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF242553; AAG31439.1; -.
DR HSSP: P22069; IONC.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; RNaseA; 1.
DR ProDom: PD000535; RNaseA; 1.
DR PROSITE: PS00127; RNase_PANCREATIC; 1.
KW Signal.
FT SIGNAL.
FT CHAIN 24 128
SQ SEQUENCE 128 AA; 14839 MW; 989719CF52053ECC CRC64;

Query Match
Best Local Similarity 66.4%; Score 383; DB 13; Length 128;
Matches 69; Conservative 11; Mismatches 24; Indels 0; Gaps 0;

OY 1 ODMLTFOKKHLTNRDVCNNILSTNLFPHCKDKNTFYISRPPEVPAICGIIASKNVLT 60
DB 24 QDMATFQKKHLTDVDDCNLMPTSLPDCCKDKNTFYISLGPVYALCRGVIFSAVDLSN 83

OY 61 SEFYSDCNVTSRPRCKYKLTSTNTFCVTCENQAPVHFVGVGHC 104
DB 84 SEFYSDCNVTSRPRCKYKLTSTNTFCVTCENQAPVHFVGVGHC 127

RESULT 5
ID Q9DFY7 PRELIMINARY; PRT; 128 AA.
AC Q9DFY7;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE RC-RNase2 ribonuclease precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
OX NCB1_Taxid=8400;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=20512555; PubMed=11058105;
RA Liao Y.D., Huang H.C., Leu Y.J., Wei C.W., Tang P.C., Wang S.C.;
RT "Purification and cloning of cytotoxic ribonucleases from Rana
RT catesbeiana (bullfrog)."
RL Nucleic Acids Res. 28:4097-4104 (2000).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RA Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF242553; AAG31439.1; -.
DR HSSP: P22069; IONC.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; RNaseA; 1.
DR ProDom: PD000535; RNaseA; 1.
DR PROSITE: PS00127; RNase_PANCREATIC; 1.
KW Signal.
FT SIGNAL.
FT CHAIN 24 128
SQ SEQUENCE 128 AA; 14839 MW; 989719CF52053ECC CRC64;

Query Match
Best Local Similarity 66.3%; Score 383; DB 13; Length 128;
Matches 69; Conservative 11; Mismatches 24; Indels 0; Gaps 0;

OY 1 ODMLTFOKKHLTNRDVCNNILSTNLFPHCKDKNTFYISRPPEVPAICGIIASKNVLT 60
DB 24 QDMATFQKKHLTDVDDCNLMPTSLPDCCKDKNTFYISLGPVYALCRGVIFSAVDLSN 83

OY 61 SEFYSDCNVTSRPRCKYKLTSTNTFCVTCENQAPVHFVGVGHC 104
DB 84 SEFYSDCNVTSRPRCKYKLTSTNTFCVTCENQAPVHFVGVGHC 127
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ID Q9DFY7 PRELIMINARY; PRT; 128 AA.
AC Q9DFY7;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE RC-RNase3 ribonuclease precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
NCBI_TaxId=8400;
RN NCBIN010000.1
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=20512555; PubMed=11058105;
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RT "Purification and cloning of cytotoxic ribonucleases from Rana
catesbeiana (bullfrog).";
RL Nucleic Acids Res. 28:4097-4104(2000).
DR HSSP; P22069; IONC.
DR InterPro: IPR001427; RNaseA.
DR Pfam; PF00074; rnaasea; 1.
DR ProDom; PD00035; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT CHAIN 1 23 POTENTIAL.
FT SIGNAL 24 128 RC-RNASE3 RIBONUCLEASE.
SQ SEQUENCE 128 AA; 14517 MW; 2B14986082E0587D CRC64;

Query Match 53.4%; Score 308; DB 13; Length 128;
Best Local Similarity 53.8%; Pred. No. 5.4e-27;
Matches 56; Conservative 13; Mismatches 35; Indels 0; Gaps 0;

QY 1 QDWLTFQKXHLTNTRDVDCNNILSTNLFHCKDKNTFYISRPVPYKAIKGIASKVLT 60
DB 24 QDWLTFQKXHLTNTRDVDCNNILSTNLFHCKDKNTFYISRPVPYKAIKGIASKVLT 60
QY 61 SEFYLSDCNVTSPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 104
DB 84 DAFLLPQCDRIKLPCHYRLDSSTNTICITCVNQPLPIHFAGVQSC 127

RESULT 6
Q9DFY5 PRELIMINARY; PRT; 128 AA.
AC Q9DFY5;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE RC-RNase6 ribonuclease precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
NCBI_TaxId=8400;
RN NCBIN010000.1
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=20512555; PubMed=11058105;
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RT "Purification and cloning of cytotoxic ribonucleases from Rana
catesbeiana (bullfrog).";
RL Nucleic Acids Res. 28:4097-4104(2000).
DR HSSP; P22069; IONC.
DR InterPro: IPR001427; RNaseA.
DR Pfam; PF00074; rnaasea; 1.
DR ProDom; PD00035; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT CHAIN 1 23 POTENTIAL.
FT SIGNAL 24 128 RC-RNASE3 RIBONUCLEASE.
SQ SEQUENCE 128 AA; 14517 MW; 2B14986082E0587D CRC64;

Query Match 53.4%; Score 308; DB 13; Length 128;
Best Local Similarity 53.8%; Pred. No. 5.4e-27;
Matches 56; Conservative 13; Mismatches 35; Indels 0; Gaps 0;

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KW Signal.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 128 RC-RNASE6 RIBONUCLEASE.
SQ SEQUENCE 128 AA; 14804 MW; AFE8FD67D266C7C2 CRC64;

Query Match 53.0%; Score 306; DB 13; Length 128;
Best Local Similarity 52.9%; Pred. No. 9.1e-27;
Matches 55; Conservative 14; Mismatches 35; Indels 0; Gaps 0;

QY 1 QDWLTFQKXHLTNTRDVDCNNILSTNLFHCKDKNTFYISRPVPYKAIKGIASKVLT 60
DB 24 QDWLTFQKXHLTNTRDVDCNNILSTNLFHCKDKNTFYISRPVPYKAIKGIASKVLT 60
QY 61 SEFYLSDCNVTSPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 104
DB 84 DVFYLPQCNRRKLPCHYRLDSSTNTICITCVNKEPLPIHFAGVQKC 127

RESULT 7
Q98SMO PRELIMINARY; PRT; 133 AA.
AC Q98SMO;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE RNase A-type ribonuclease rc208 precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
NCBI_TaxId=8400;
RN NCBIN010000.1
RP SEQUENCE FROM N.A.
RX MEDLINE=21539506; PubMed=11683320;
RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT "Rapid diversification of RNase A superfamily ribonucleases from the
bullfrog, Rana catesbeiana.";
RL J. Mol. Evol. 53:31-38(2001).
DR EMBL; AF351209; AAK30255.1; -.
DR HSSP; P1916; IBC4.
DR InterPro: IPR001427; RNaseA.
DR Pfam; PF00074; rnaasea; 1.
DR ProDom; PD00035; RNaseA; 1.
DR SMART; SM00092; RNase PC; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL 1 22 POTENTIAL.
FT SIGNAL 23 133 RC-RNASE6 RIBONUCLEASE.
SQ SEQUENCE 133 AA; 14628 MW; 87FCF122C3499E02 CRC64;

Query Match 51.1%; Score 295; DB 13; Length 133;
Best Local Similarity 48.6%; Pred. No. 1.6e-25;
Matches 54; Conservative 17; Mismatches 32; Indels 8; Gaps 3;

QY 1 QDWLTFQKXHLTNTRDVDCNNILSTNLFHCKDKNTFYISRPVPYKAIKGIASKVLT 56
DB 23 QDWLTFQKXHLTNTRDVDCNNILSTNLFHCKDKNTFYISRPVPYKAIKGIASKVLT 56
QY 57 VLTSTSEFYLSDC--NVTSPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 104
DB 82 VLTSTSEFYLSDC--NVTSPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 104

RESULT 8
Q9PWR7 PRELIMINARY; PRT; 133 AA.
AC Q9PWR7;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE RNase A-type ribonuclease precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
NCBI_TaxId=8400;
RN NCBIN010000.1
RP SEQUENCE FROM N.A.
RX MEDLINE=20512555; PubMed=11058105;
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RT "Purification and cloning of cytotoxic ribonucleases from Rana
catesbeiana (bullfrog).";
RL Nucleic Acids Res. 28:4097-4104(2000).
DR HSSP; P22069; IONC.
DR InterPro: IPR001427; RNaseA.
DR Pfam; PF00074; rnaasea; 1.
DR ProDom; PD00035; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT CHAIN 1 23 POTENTIAL.
FT SIGNAL 24 128 RC-RNASE3 RIBONUCLEASE.
SQ SEQUENCE 128 AA; 14517 MW; 2B14986082E0587D CRC64;

Query Match 53.4%; Score 308; DB 13; Length 128;
Best Local Similarity 53.8%; Pred. No. 5.4e-27;
Matches 56; Conservative 13; Mismatches 35; Indels 0; Gaps 0;

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OK NCBI_TaxID=8400;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=98165825; PubMed=9497370;
 RA Huang H.C., Wang S.C., Leu Y.J., Lu S.C., Liao Y.D.;
 RT "The Rana catesbeiana rcr gene encoding a cytotoxic ribonuclease.
 RT Tissue distribution, cloning, purification, cytotoxicity, and active
 RT residue for RNase activity.";
 RL J. Biol. Chem. 273:6395-6401(1998).
 DR EMBL: AF039104; AAD10702.1; -.
 DR HSSP: P11916; 1BC4.
 DR InterPro: IPR001427; RNaseA.
 DR Pfam: PF00074; rnasea; 1.
 DR ProDom: PD000535; RNaseA; 1.
 DR SMART: SM00092; RNase_Pc; 1.
 DR PROSITE: PS00127; RNASE_PANCREATIC; 1.
 KM Signal.
 FT SIGNAL.
 FT CHAIN.
 SQ SEQUENCE 133 AA; 14762 MW; A7D62594F7D16F0C CRC64;

Query Match 50.1%; Score 289; DB 13; Length 133;
 Best Local Similarity 48.6%; Pred. No. 7, 8e-25;
 Matches 54; Conservative 17; Mismatches 32; Indels 8; Gaps 3;

QY 1 QDWLTFOKHGTLNTRDVCNNILSTNLF---HCKDKNTFIYSRPPVKAICKGIASKN 56
 DB 23 QWMAFQOQHINTPIINCNTIMDNNIYIVGGCKKVNFIISATTVAIKCTGVI-NMN 81
 QY 57 VLTSEFYLSDC--NVTSRPCKYKUKKSTNTFCVTCENQAPVHPVGVGHC 104
 DB 82 VLSPTRFQDLCTRTSITRPPCPYSSRTETNYICVCKENQVPVHPAGIGKC 132

RESULT 9
 Q98SL9 PRELIMINARY; PRT; 133 AA.
 AC Q98SL9;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE RNase A-type ribonuclease rc212 precursor.
 OS Rana catesbeiana (Bull frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
 OC NCBI_TaxID=8400;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21539506; PubMed=11683320;
 RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
 RT "Rapid diversification of RNase A superfamily ribonuclease from the
 RT bullfrog, *Rana catesbeiana*.";
 RL J. Mol. Evol. 53:31-38(2001).
 DR EMBL: AF351210; AAK30256.1; -.
 DR HSSP: P11916; 1BC4.
 DR InterPro: IPR001427; RNaseA.
 DR Pfam: PF00074; rnasea; 1.
 DR ProDom: PD000535; RNaseA; 1.
 DR SMART: SM00092; RNase_Pc; 1.
 DR PROSITE: PS00127; RNASE_PANCREATIC; 1.
 KM Signal.
 FT SIGNAL.
 FT CHAIN.
 SQ SEQUENCE 133 AA; 14615 MW; C8785B26B26E54E CRC64;

Query Match 49.0%; Score 283; DB 13; Length 133;
 Best Local Similarity 46.8%; Pred. No. 3, 7e-24;
 Matches 52; Conservative 18; Mismatches 33; Indels 8; Gaps 3;

QY 1 QDWLTFOKHGTLNTRDVCNNILSTNLF---HCKDKNTFIYSRPPVKAICKGIASKN 56
 DB 23 QWMAFQOQHINTPIINCNTIMDNNIYIVGGCKKVNFIISATTVAIKCTGVI-NMN 81

QY 57 VLTSEFYLSDC--NVTSRPCKYKUKKSTNTFCVTCENQAPVHPVGVGHC 104
 DB 82 VLSPTRFQDLCTRTSITRPPCPYSSRTETNYICVCKENQVPVHPAGIGKC 132

RESULT 10
 Q98SM2 PRELIMINARY; PRT; 132 AA.
 AC Q98SM2;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE RNase A-type ribonuclease rc203 precursor (RC-RNase7 precursor).
 OS Rana catesbeiana (Bull frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
 OC NCBI_TaxID=8400;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21539506; PubMed=11683320;
 RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
 RT "Rapid diversification of RNase A superfamily ribonuclease from the
 RT bullfrog, *Rana catesbeiana*.";
 RL J. Mol. Evol. 53:31-38(2001).
 DR EMBL: AF351207; AAK30253.1; -.
 DR HSSP: P11916; 1BC4.
 DR InterPro: IPR001427; RNaseA.
 DR Pfam: PF00074; rnasea; 1.
 DR ProDom: PD000535; RNaseA; 1.
 DR SMART: SM00092; RNase_Pc; 1.
 DR PROSITE: PS00127; RNASE_PANCREATIC; 1.
 KM Signal.
 FT SIGNAL.
 FT CHAIN.
 SQ SEQUENCE 132 AA; 14412 MW; 131A745187978687 CRC64;

Query Match 48.9%; Score 282; DB 13; Length 132;
 Best Local Similarity 46.8%; Pred. No. 4, 7e-24;
 Matches 52; Conservative 15; Mismatches 36; Indels 8; Gaps 3;

QY 1 QDWLTFOKHGTLNTRDVCNNILSTNLF---HCKDKNTFIYSRPPVKAICKGIASKN 56
 DB 23 QWMAFQOQHINTPIINCNTIMDNNIYIVGGCKKVNFIISATTVAIKCTGVI-NMN 81
 QY 57 VLTSEFYLSDC--NVTSRPCKYKUKKSTNTFCVTCENQAPVHPVGVGHC 104
 DB 82 VLSPTRFQDLCTRTSITRPPCPYSSKKTETNYICVCKENQVPVHPAGIGKC 132

RESULT 11
 Q98SL8 PRELIMINARY; PRT; 133 AA.
 AC Q98SL8;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE RNase A-type ribonuclease rc218 precursor.
 OS Rana catesbeiana (Bull frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
 OC NCBI_TaxID=8400;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21539506; PubMed=11683320;
 RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
 RT "Rapid diversification of RNase A superfamily ribonuclease from the
 RT bullfrog, *Rana catesbeiana*.";

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RL J. Mol. Evol. 53:31-38(2001).
DR EMBL: AF351211; AAK30257.1; -.
DR HSP: P11916; 1BC4.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; rnaaseA; 1.
DR ProDom: PD000535; RNaseA; 1.
DR SMART: SM00092; RNase_Pc; 1.
DR PROSITE: PS00127; RNASE_PANCREATIC; 1.
KM Signal.
FT SIGNAL.
SQ SEQUENCE 133 AA; 14590 MW; 8B40B9A9FA5B943 CRC64;
  1 22 POTENTIAL.
Query Match 48.4%; Score 279; DB 13; Length 132;
Best Local Similarity 45.9%; Pred. No. 1e-23;
Matches 51; Conservative 19; Mismatches 33; Indels 8; Gaps 3;
  1 57 VLTSEFYLSDCN---VTSRPCKYKLTGSTNTFCVTCENQAPVHFGVGHG 104
  23 QWMATFQEQHITNTSSINIMNSLYIVGGQCKKVNFIASSATVVGICSG-VTDKK 81
  57 VLTSEFYLSDCN---VTSRPCKYKLTGSTNTFCVTCENQAPVHFGVGHG 104
  82 VLSTKFLDICTRIETPRPCPYSSRTETNYICVCKENQYVHFGAGIGC 132
RESULT 12
ID 098SM1 PRELIMINARY; PRT; 132 AA.
AC 098SM1;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE RNase A-type ribonuclease rc204 precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.
OX NCBI_TaxID=8400;
  1 11
RN SIGNAL.
RP MEDLINE=21539506; Pubmed=11683320;
RX Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT "Rapid diversification of RNase A superfamily ribonuclease from the
RT bullfrog, Rana catesbeiana.";
RL J. Mol. Evol. 53:31-38(2001).
DR EMBL: AF351208; AAK30254.1; -.
DR HSP: P11916; 1BC4.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; rnaaseA; 1.
DR ProDom: PD000535; RNaseA; 1.
DR SMART: SM00092; RNase_Pc; 1.
DR PROSITE: PS00127; RNASE_PANCREATIC; 1.
KM Signal.
FT SIGNAL.
SQ SEQUENCE 132 AA; 14704 MW; 95D61760F729868E CRC64;
  1 22 POTENTIAL.
Query Match 48.0%; Score 277; DB 13; Length 132;
Best Local Similarity 47.7%; Pred. No. 1.7e-23;
Matches 53; Conservative 15; Mismatches 35; Indels 8; Gaps 3;
  1 57 VLTSEFYLSDCN---VTSRPCKYKLTGSTNTFCVTCENQAPVHFGVGHG 104
  23 QWMPFQCKHITNTSSICNTIMDDIYIVGGQCKKVNFIYSATVKAICTGVANS-N 81
  57 VLTSEFYLSDCN---VTSRPCKYKLTGSTNTFCVTCENQAPVHFGVGHG 104
  82 VLSTTRFOLXXTRIFITSRCPYSSRTETNYICVCKENQYVHFGAGIGC 132
RESULT 13
ID 09DF78 PRELIMINARY; PRT; 132 AA.
AC 09DF78;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
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DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE RC-RNaseB1 ribonuclease precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
OX NCBI_TaxID=8400;
  1 11
RN SIGNAL.
RP MEDLINE=20512555; Pubmed=11058105;
RX Liao Y.-D., Huang H.-C., Liao Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RT "Purification and cloning of cytotoxic ribonucleases from Rana
RT catesbeiana (bullfrog).";
RL Nucleic Acids Res. 28:4097-4104(2000).
  1 21 POTENTIAL.
RN SIGNAL.
RP TISSUE=Liver;
RC TISSUE=Liver;
RX MEDLINE=20512555; Pubmed=11058105;
RA Liao Y.-D., Huang H.-C., Liao Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RT Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL: AF288642; AAG30414.2; -.
DR HSP: P11916; 1BC4.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; rnaaseA; 1.
DR ProDom: PD000535; RNaseA; 1.
DR SMART: SM00092; RNase_Pc; 1.
DR PROSITE: PS00127; RNASE_PANCREATIC; 1.
KM Signal.
FT SIGNAL.
SQ SEQUENCE 132 AA; 14625 MW; DB99A517452FBE53 CRC64;
  1 21 POTENTIAL.
  22 RC-RNASEB1 RIBONUCLEASE.
  132
  14625 MW; DB99A517452FBE53 CRC64;
Query Match 47.2%; Score 272.5; DB 13; Length 132;
Best Local Similarity 43.2%; Pred. No. 5.6e-23;
Matches 48; Conservative 20; Mismatches 36; Indels 7; Gaps 2;
  1 57 VLTSEFYLSDCN---VTSRPCKYKLTGSTNTFCVTCENQAPVHFGVGHG 104
  22 QWMAFKKHTTSSIDCNTIMDAIYIVGGQCKKNTFTISSDNNKALICSGVSPDK 81
  57 VLTSEFYLSDCN---VTSRPCKYKLTGSTNTFCVTCENQAPVHFGVGHG 104
  82 ELSTSPFLNCTIRDSIRPRCPYHSPDNNKIKVCKEQLPVHFGVGHG 132
RESULT 14
ID 09W738 PRELIMINARY; PRT; 169 AA.
AC 09W738;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE FRL2 protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodidae; Xenopus.
OX NCBI_TaxID=8355;
  1 11
RN SIGNAL.
RP MEDLINE=96069863; Pubmed=7585965;
RX Kirschner M.W., Minshall J., Kirschner M.W.;
RT "The identification of two novel ligands of the FGF receptor by a
RT yeast screening method and their activity in Xenopus development.";
RL Cell 83:621-630(1995).
  1 21
RN SIGNAL.
RP Kirschner M.W.;
RA Kirschner M.W.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF159166; AAD41901.1; -.
DR HSP: P00656; 1LSO.
DR InterPro: IPR001427; RNaseA.
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DR Pfam: PF00074; rnaaseA; 1.
DR ProDom: PD000535; RnaaseA; 1.
DR ProSITE: PS00127; Rnaase_PANCREATIC; 1.
SQ SEQUENCE 169 AA; 18851 MW; D969F3E43B3CE1B8 CRC64;

Query Match 27.1%; Score 156.5; DB 13; Length 169;
Best Local Similarity 36.1%; Pred. No. 8.3e-10;
Matches 39; Conservative 19; Mismatches 35; Indels 15; Gaps 6;

QY 6 FOKKHULTNT-RDVDCN-----NILSTNLFHCKDKNTFIY-SRPEPVKAICKGIISKNV 57
DB 33 FWEKXIVVEGATNCNQTIKDKNIRFKN-NCKFRFTFIHDTNGKVKVCKEMCAGIVKSTFV 90

QY 58 LTTSEFVLSDCNV---TSRP--CKYKLKSTNTFCVTCENQAPVHPVG 100
DB 91 ISKELLPLTDCLMGRTARPPNCAYNQTRTGTGINITCENNYFVHPFAG 138

RESULT 15

Q9JKI9 PRELIMINARY; PRT; 157 AA.

AC Q9JKI9; 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)

DE Eosinophil-associated ribonuclease 44.

GN EAR44.

OS Meriones unguiculatus (Mongolian jird) (Mongolian gerbil).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;

OC Meriones.

OK NCBI_TaxID=10047;

RN (1)

RP SEQUENCE FROM N.A.

RX MEDLINE=20243759; PubMed=10758160;

RA Zhang J., Dyer K.D., Rosenberg H.F.;

RT "Evolution of the rodent eosinophil-associated ribonuclease gene

family by rapid gene sorting and positive selection.";

RL Proc. Natl. Acad. Sci. U.S.A. 97:4701-4706(2000).

DR EMBL; AF236394; AAF67694.1; -.

DR HSSP; P10153; 1H12.

DR InterPro: IPR001427; RnaaseA.

Pfam: PF00074; rnaaseA; 1.

DR ProDom: PD000535; RnaaseA; 1.

DR SMART; SM00092; Rnaase_Pc; 1.

DR PROSITE; PS00127; Rnaase_PANCREATIC; 1.

SQ SEQUENCE 157 AA; 17887 MW; 34FE2AE777EF3709 CRC64;

Query Match 22.2%; Score 128; DB 11; Length 157;

Best Local Similarity 30.3%; Pred. No. 1.3e-06;

Matches 33; Conservative 21; Mismatches 35; Indels 20; Gaps 7;

QY 3 WLTFOKHULTNTRDVDCN-NILSTNLF-HCKDKNTFIYSRPEPV-----KAICKGI 52
DB 36 WFTIQ--HISNTTTCQNAAMLGNNVYTGRCQDLNFTLHTRFANVNECVNRTTCKN-- 91

QY 53 ASKNVU-TSEFVLSDCNVTS-----RPCKYKLKSTNTFCVTCENQAP 95
DB 92 GRNCHDSRSKVSITDCNLTSPSANYRQCRYQRTARKFYRIACNNKTP 140

Search completed: January 22, 2004, 12:08:50
Job time : 25.7079 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 22, 2004, 12:01:20 (Search time 33.0337 Seconds
(without alignments)
504.524 Million cell updates/sec

Title: US-09-622-613C-8
Perfect score: 580
Sequence: 1 MQDWLTFQKGLTNRDVDC.....TFCVTCENQAPVHFVGVGHC 105

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: A_GeneSeq_19Jun03:*

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- 2: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/AA1981.DAT:*
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- 19: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/AA1998.DAT:*
- 20: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/AA1999.DAT:*
- 21: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/AA2000.DAT:*
- 22: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/AA2001.DAT:*
- 23: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/AA2002.DAT:*
- 24: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	573	98.8	105	20	AA19869
2	571	98.4	105	20	AA19867
3	568	97.9	104	20	AA19866
4	566	97.6	104	20	AA19865
5	566	97.6	105	20	AA19871
6	566	97.6	127	20	AA19879
7	561	96.7	104	20	AA19870
8	546	94.1	104	18	AAW06544
9	546	94.1	105	18	AAW35123

10	546	94.1	105	20	AA199400	Recombinant frog O
11	546	94.1	355	18	AAW35125	R. pipiens recombi
12	546	94.1	358	18	AAW35130	R. pipiens recombi
13	544	93.8	104	14	AAW30301	Recombinant onc pr
14	544	93.8	104	22	AAW31666	Amino acid sequenc
15	544	93.8	104	23	ABG32650	Northern leopard f
16	544	93.8	112	18	AAW35118	R. pipiens recombi
17	544	93.8	251	18	AAW35134	R. pipiens recombi
18	544	93.8	254	18	AAW35135	R. pipiens recombi
19	544	93.8	355	18	AAW35129	R. pipiens recombi
20	544	93.8	355	18	AAW35133	R. pipiens recombi
21	544	93.8	366	18	AAW35132	R. pipiens recombi
22	544	93.8	379	18	AAW35126	R. pipiens recombi
23	543	93.6	104	18	AAW30302	Recombinant onc pr
24	541	93.3	104	12	AAW12344	Protein with activ
25	541	93.3	104	15	AAW47303	ONCONASE (pharmace
26	541	93.3	104	17	AAW00736	Protein derived fr
27	541	93.3	104	18	AAW06543	Autitumour protein
28	541	93.3	104	18	AAW14065	Onconase (RTM) pro
29	541	93.3	104	20	AAW33322	Frog onconase prot
30	541	93.3	104	20	AAW88233	Rana pipiens RNase
31	541	93.3	104	22	AAW31667	Amino acid sequenc
32	541	93.3	104	23	ABG31617	Northern leopard f
33	539	92.9	105	18	AAW35116	R. pipiens recombi
34	539	92.9	106	18	AAW35122	R. pipiens recombi
35	539	92.9	107	18	AAW35117	R. pipiens recombi
36	538	92.8	105	18	AAW35115	R. pipiens recombi
37	536	92.4	104	18	AAW18224	Autitumour genetic
38	535	92.2	358	18	AAW35127	R. pipiens recombi
39	535	92.2	365	18	AAW35131	R. pipiens recombi
40	516	89.0	107	18	AAW35120	R. pipiens recombi
41	483	83.3	360	18	AAW35128	R. pipiens recombi
42	471.5	81.3	111	18	AAW35121	R. pipiens recombi
43	433	74.7	83	20	AAW35119	R. pipiens clone R
44	433	74.7	83	20	AAW88234	Rana pipiens RNase
45	277	47.8	111	20	AAW33321	Frog lectin protei

ALIGNMENTS

RESULT 1	AA19869	AA19869 standard; Protein, 105 AA.
AC	AA19869;	
XX		
DT	25-JAN-2000 (first entry)	
XX		
DE	Recombinant Met(-1) RapLRI Met23Jleu-(His)6 protein.	
XX		
KW	Recombinant Met(-1) Rana pipiens ribonuclease Met23Jleu-(His)6; RapLRI;	
KW	CD22; covalently bound; IL2 antibody; ligand binding moiety; RNase;	
KW	cancerous B cell; Kapos'i's sarcoma; human chorionic gonadotropin; hCG;	
KW	signal peptide; recombinant ribonuclease; cytotoxic fusion protein;	
KW	cancer; frog; autoimmune disease.	
OS	Rana pipiens.	
OS	Synthetic.	
XX		
FT	Key	Location/Qualifiers
FT	Misc-difference 1	/note= "(His)6 histidine tag attached to N-terminal Met"
FT	Misc-difference 1	/note= "Met not found in wild type RapLRI"
FT	Misc-difference 24	/note= "Wild type Met replaced with Leu"
XX		
PN	MO9950398-A2.	
XX		
XX	07-OCT-1999.	
PD		
XX		
PF	26-MAR-1999;	99WO-US06641.

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XX 27-MAR-1998; 98US-0079751.
PR (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Newton DL, Rybak SM;
XX MPI; 1999-610847/52.
XX N-PSDB; AA208127.
XX
XX New recombinant ribonucleases, used for killing target cells, e.g. for
XX treating cancers, viral infections or autoimmune diseases.
XX
XX Claim 4; Page 59; 71pp; English.
XX
XX The present sequence is a recombinant Rana pipiens ribonuclease protein
XX (RapLRL) with Met at position 1 attached to (His)6 tag and Met24Leu.
XX Carboxy terminal end of recombinant RapLRL has a covalently bound ligand
XX binding moiety, which can be a LL2 antibody directed against CD22 on
XX cancerous B cells or human chorionic gonadotropin (hCG) effective
XX against Kaposi's sarcoma cells. Recombinant ribonucleases can be
XX expressed in bacteria without an N-terminal methionine due to the
XX presence of a signal peptide that is cleaved by bacteria. The soluble
XX expression of ribonuclease allows the proteins to be fused in-frame with
XX ligand binding moieties to form cytotoxic fusion proteins. They can be
XX used for treatment of cancer and autoimmune diseases.
XX
XX Sequence 105 AA;
SQ
XX
XX Query Match 98.8%; Score 573; DB 20; Length 105;
XX Best Local Similarity 99.0%; Pred. No. 3,2e-61;
XX Matches 104; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 MODMLTFQKKHLTNTRDVDCNNILSTNLFHCKDKNTFTYSRPEPVAKICKGIASKNVLT 60
XX |||||
XX 1 MODMLTFQKKHLTNTRDVDCNNILSTNLFHCKDKNTFTYSRPEPVAKICKGIASKNVLT 60
XX
XX QY 61 TSEFYLSDCNVTSRPCKYKTKKSTITFCVTCENQAPVHFGVGHG 105
XX |||||
XX 61 TSEFYLSDCNVTSRPCKYKTKKSTITFCVTCENQAPVHFGVGHG 105
XX
XX Db
XX
XX RESULT 2
XX AAY28867
XX ID AAY28867 standard; Protein; 105 AA.
XX
XX AC AAY28867;
XX
XX DT 25-JAN-2000 (first entry)
XX
XX DE Recombinant Met(-1) RapLRL.
XX
XX KW Recombinant Met(-1) Rana pipiens ribonuclease; RapLRL; CD22; RNase;
XX covalently bound; LL2 antibody; ligand binding moiety; cancerous B cell;
XX Kaposi's sarcoma; human chorionic gonadotropin; hCG; signal peptide;
XX recombinant ribonuclease; cytotoxic fusion protein; cancer; frog;
XX autoimmune disease.
XX
XX OS Rana pipiens.
XX Synthetic.
XX
XX Key Location/Qualifiers
XX FT Misc-difference 1 /note= "Met not found in wild type RapLRL"
XX FT
XX PN WO9950398-A2.
XX
XX PD 07-OCT-1999.
XX
XX PF 26-MAR-1999; 99WO-US06641.
XX
XX PR 27-MAR-1998; 98US-0079751.
XX
XX

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PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Newton DL, Rybak SM;
XX MPI; 1999-610847/52.
XX N-PSDB; AA208126.
XX
XX New recombinant ribonucleases, used for killing target cells, e.g. for
XX treating cancers, viral infections or autoimmune diseases.
XX
XX Claim 34; Page 57; 71pp; English.
XX
XX The present sequence is a recombinant Rana pipiens ribonuclease (RapLRL)
XX protein with Met at position 1. Carboxy terminal end of recombinant
XX RapLRL has a covalently bound ligand binding moiety, which can be a LL2
XX antibody directed against CD22 on cancerous B cells or human chorionic
XX gonadotropin (hCG) effective against Kaposi's sarcoma cells. Recombinant
XX ribonucleases can be expressed in bacteria without an N-terminal
XX methionine due to the presence of a signal peptide that is cleaved by
XX bacteria. The soluble expression of ribonuclease allows the proteins to
XX be fused in-frame with ligand binding moieties to form cytotoxic fusion
XX proteins. They can be used for treatment of cancer and autoimmune
XX diseases.
XX
XX Sequence 105 AA;
SQ
XX
XX Query Match 98.4%; Score 571; DB 20; Length 105;
XX Best Local Similarity 98.1%; Pred. No. 5,5e-61;
XX Matches 103; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 MODMLTFQKKHLTNTRDVDCNNILSTNLFHCKDKNTFTYSRPEPVAKICKGIASKNVLT 60
XX |||||
XX 1 MODMLTFQKKHLTNTRDVDCNNIMSTNLFHCKDKNTFTYSRPEPVAKICKGIASKNVLT 60
XX
XX Db
XX
XX QY 61 TSEFYLSDCNVTSRPCKYKTKKSTITFCVTCENQAPVHFGVGHG 105
XX |||||
XX 61 TSEFYLSDCNVTSRPCKYKTKKSTITFCVTCENQAPVHFGVGHG 105
XX
XX Db
XX
XX RESULT 3
XX AAY28866
XX ID AAY28866 standard; Protein; 104 AA.
XX
XX AC AAY28866;
XX
XX DT 25-JAN-2000 (first entry)
XX
XX DE Recombinant RapLRL Met23Leu amino acid sequence.
XX
XX KW Recombinant Rana pipiens ribonuclease; RapLRL Met23Leu; covalently bound;
XX LL2 antibody; ligand binding moiety; CD22; cancerous B cell; RNase;
XX Kaposi's sarcoma; human chorionic gonadotropin; hCG; signal peptide;
XX recombinant ribonuclease; cytotoxic fusion protein; cancer; frog;
XX autoimmune disease.
XX
XX OS Rana pipiens.
XX Synthetic.
XX
XX Key Location/Qualifiers
XX FT Misc-difference 23 /note= "Wild type Met replaced with Leu"
XX FT
XX PN WO9950398-A2.
XX
XX PD 07-OCT-1999.
XX
XX PF 26-MAR-1999; 99WO-US06641.
XX
XX PR 27-MAR-1998; 98US-0079751.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX Newton DL, Rybak SM;
XX

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XX WPI: 1999-610847/52.
 DR N-PSDB; AA208125.
 XX
 PT New recombinant ribonucleases, used for killing target cells, e.g. for
 PS treating cancers, viral infections or autoimmune diseases -
 XX
 PS Claim 34; Page 56; 71pp; English.
 CC The present sequence is a recombinant Rana pipiens ribonuclease (RapLr1)
 CC protein with Met33Leu. Carboxy terminal end of recombinant RapLr1 has a
 CC covalently bound ligand binding moiety, which can be a L12 antibody
 CC gonadotrophin (hCG) effective against Kaposi's sarcoma cells. Recombinant
 CC ribonucleases can be expressed in bacteria without an N-terminal
 CC methionine due to the presence of a signal peptide that is cleaved by
 CC bacteria. The soluble expression of ribonucleases allows the proteins to
 CC be fused in-frame with ligand binding moieties to form cytotoxic fusion
 CC proteins. They can be used for treatment of cancer and autoimmune
 CC diseases.
 XX
 SQ Sequence 104 AA;
 Query Match 97.9%; Score 568; DB 20; Length 104;
 Best Local Similarity 99.0%; Pred. No. 1.3e-60;
 Matches 103; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 2 ODMLTFOKKHLNTRDVCNNILSTNLFHCKDKNTFISRPPEPVAKICKGIASKNVLT 61
 DB 1 ODMLTFOKKHLNTRDVCNNILSTNLFHCKDKNTFISRPPEPVAKICKGIASKNVLT 60
 OY 62 SEFYLSDCNVTSRPCKYKYLKSTITFCVTCENQAPVHFVGHC 105
 DB 61 SEFYLSDCNVTSRPCKYKYLKSTITFCVTCENQAPVHFVGHC 104
 RESULT 4
 AAY28865
 ID AAY28865 standard; Protein; 104 AA.
 XX
 AC AAY28865;
 XX
 DT 25-JAN-2000 (first entry)
 XX
 DE Rana pipiens liver ribonuclease (RapLr1).
 XX
 KM Rana pipiens liver ribonuclease; RapLr1; covalently bound; L12 antibody;
 KM ligand binding moiety; CD22; cancerous B cell; Kaposi's Sarcoma; frog;
 KM human chorionic gonadotrophin; hCG; recombinant ribonuclease; RNase;
 KM signal peptide; cytotoxic fusion protein; cancer; autoimmune disease.
 XX
 OS Rana pipiens.
 XX
 PN WO9950398-A2.
 XX
 PD 07-OCT-1999.
 XX
 PF 26-MAR-1999; 99WO-US06641.
 XX
 PR 27-MAR-1998; 98US-0079751.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Newton DL, Rybak SM;
 XX
 DR WPI: 1999-610847/52.
 XX
 DR N-PSDB; AA208124.
 XX
 PT New recombinant ribonucleases, used for killing target cells, e.g. for
 PT treating cancers, viral infections or autoimmune diseases -
 XX
 PS Claim 1; Page 55; 71pp; English.

CC The present sequence is Rana pipiens liver ribonuclease (RapLr1)
 CC protein. Carboxy terminal end of RapLr1 has a covalently bound
 CC ligand binding moiety, which can be a L12 antibody directed against
 CC CD22 on cancerous B cells or human chorionic gonadotrophin (hCG)
 CC effective against Kaposi's Sarcoma cells. Recombinant ribonucleases can
 CC be expressed in bacteria without an N-terminal methionine due to the
 CC presence of a signal peptide that is cleaved by bacteria. The soluble
 CC expression of ribonuclease allows the proteins to be fused in-frame with
 CC ligand binding moieties to form cytotoxic fusion proteins. They can be
 CC used for treatment of cancer and autoimmune diseases.
 XX
 SQ Sequence 104 AA;
 Query Match 97.6%; Score 566; DB 20; Length 104;
 Best Local Similarity 98.1%; Pred. No. 2.2e-60;
 Matches 102; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 OY 2 ODMLTFOKKHLNTRDVCNNILSTNLFHCKDKNTFISRPPEPVAKICKGIASKNVLT 61
 DB 1 ODMLTFOKKHLNTRDVCNNILSTNLFHCKDKNTFISRPPEPVAKICKGIASKNVLT 60
 OY 62 SEFYLSDCNVTSRPCKYKYLKSTITFCVTCENQAPVHFVGHC 105
 DB 61 SEFYLSDCNVTSRPCKYKYLKSTITFCVTCENQAPVHFVGHC 104
 RESULT 5
 AAY28871
 ID AAY28871 standard; Protein; 105 AA.
 XX
 AC AAY28871;
 XX
 DT 25-JAN-2000 (first entry)
 XX
 DE Recombinant Met(-1) RapLr1 GlnSer amino acid sequence.
 XX
 KM Recombinant Met(-1) Rana pipiens ribonuclease GlnSer; RapLr1; CD22;
 KM covalently bound; L12 antibody; ligand binding moiety; cancerous B cell;
 KM Kaposi's sarcoma; human chorionic gonadotrophin; hCG; signal peptide;
 KM recombinant ribonuclease; cytotoxic fusion protein; cancer; frog;
 KM autoimmune disease; RNase.
 XX
 OS Rana pipiens.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1 /note= "Met not found in wild type RapLr1"
 FT Misc-difference 2 /note= "wild type Gln replaced with Ser"
 FT
 XX
 PN WO9950398-A2.
 XX
 PD 07-OCT-1999.
 XX
 PF 26-MAR-1999; 99WO-US06641.
 XX
 PR 27-MAR-1998; 98US-0079751.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Newton DL, Rybak SM;
 XX
 DR WPI: 1999-610847/52.
 XX
 DR N-PSDB; AA208129.
 XX
 PT New recombinant ribonucleases, used for killing target cells, e.g. for
 PT treating cancers, viral infections or autoimmune diseases -
 XX
 PS Claim 34; Page 61; 71pp; English.
 CC The present sequence is a recombinant Rana pipiens ribonuclease (RapLr1)
 CC protein with Met at position 1 and GlnSer. Carboxy terminal end of

recombinant RAPLRI has a covalently bound ligand binding moiety, which can be a IL2 antibody directed against CD22 on cancerous B cells or human chorionic gonadotrophin (hCG) effective against Kaposi's sarcoma cells. Recombinant ribonucleases can be expressed in bacteria without an N-terminal methionine due to the presence of a signal peptide that is cleaved by bacteria. The soluble expression of ribonuclease allows the proteins to be fused in-frame with ligand binding moieties to form cytotoxic fusion proteins. They can be used for treatment of cancer and autoimmune diseases.

Sequence 105 AA;

Query Match 97.6%; Score 566; DB 20; Length 105;

Best Local Similarity 97.1%; Pred. No. 2.2e-60; Mismatches 1; Indels 0; Gaps 0;

Matches 102; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

1 MODMLTFQKKHLTNTRDVCNNILSTNLFPHCKDKNTFTISRPEPVAKIGIIASKNVLT 60
1 MSDMLTFQKKHLTNTRDVCNNIMSTNLFHCKDKNTFTISRPEPVAKIGIIASKNVLT 60

61 TSEFYISDCNVTSRPCKYKLLKSTTFTCYTCENQAPVHFVGVC 105
61 TSEFYISDCNVTSRPCKYKLLKSTTFTCYTCENQAPVHFVGVC 105

RESULT 6
AA28879 standard; Protein; 127 AA.

AA28879; AAY28879; 25-JAN-2000 (first entry)

Rana pipiens Clone 5a1b ribonuclease.

Rana pipiens ribonuclease Clone 5a1b; RAPLRI; covalently bound; RNase; IL2 antibody; ligand binding moiety; CD22; cancerous B cell; oncogene; Kaposi's Sarcoma; human chorionic gonadotrophin; hCG; cancer; recombinant ribonuclease; frog; signal peptide; cytotoxic fusion protein; autoimmune disease.

Rana pipiens.

Key Location/Qualifiers

FT Peptide 1..23 /label= Signal_peptide

FT Protein 24..127 /note= "putative"

FT /label= Rana_pipiens_Clone_5a1b_ribonuclease

PN MO9950398-A2.

PD 07-OCT-1999.

PF 26-MAR-1999; 99WO-US06641.

PR 27-MAR-1998; 98US-0079751.

(USSH) US DEPT HEALTH & HUMAN SERVICES.

PA Newton DL, Rybak SM;

PI MPI; 1999-610847/52.

DR N-PSDB; AA208136.

PT New recombinant ribonucleases, used for killing target cells, e.g. for treating cancers, viral infections or autoimmune diseases -

PS Disclosure; Page 69; 71pp; English.

CC The present sequence is a Rana pipiens Clone 5a1b ribonuclease (RAPLRI). It is encoded by clone 5a1b cDNA obtained from Rana pipiens liver mRNA library. It exhibits differences with Oncogene (RTM) at amino acid

residues 11, 20, 85 and 103. Carboxy terminal end of RAPLRI has a covalently bound ligand binding moiety, which can be a IL2 antibody directed against CD22 on cancerous B cells or human chorionic gonadotrophin (hCG) effective against Kaposi's Sarcoma cells. Recombinant ribonucleases can be expressed in bacteria without an N-terminal methionine due to the presence of a signal peptide that is cleaved by bacteria. The soluble expression of ribonuclease allows the proteins to be fused in-frame with ligand binding moieties to form cytotoxic fusion proteins. They can be used for treatment of cancer and autoimmune diseases.

Sequence 127 AA;

Query Match 97.6%; Score 566; DB 20; Length 127;

Best Local Similarity 98.1%; Pred. No. 2.8e-60; Mismatches 1; Indels 0; Gaps 0;

Matches 102; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

2 QDMLTFQKKHLTNTRDVCNNILSTNLFPHCKDKNTFTISRPEPVAKIGIIASKNVLT 61
24 QDMLTFQKKHLTNTRDVCNNIMSTNLFHCKDKNTFTISRPEPVAKIGIIASKNVLT 83

62 SEFYISDCNVTSRPCKYKLLKSTTFTCYTCENQAPVHFVGVC 105
62 SEFYISDCNVTSRPCKYKLLKSTTFTCYTCENQAPVHFVGVC 105

84 SEFYISDCNVTSRPCKYKLLKSTTFTCYTCENQAPVHFVGVC 127

RESULT 7
AA28870 standard; Protein; 104 AA.

AA28870; AAY28870; 25-JAN-2000 (first entry)

Recombinant RAPLRI Glniser amino acid sequence.

Recombinant Rana pipiens ribonuclease; RAPLRI Glniser; covalently bound; IL2 antibody; ligand binding moiety; CD22; cancerous B cell; frog; Kaposi's sarcoma; human chorionic gonadotrophin; hCG; signal peptide; recombinant ribonuclease; cytotoxic fusion protein; cancer; RNase; autoimmune disease.

Rana pipiens.

Key Location/Qualifiers

FT Misc-difference 1 /note= "Wild type Gln replaced with Ser"

PN MO9950398-A2.

PD 07-OCT-1999.

PF 26-MAR-1999; 99WO-US06641.

PR 27-MAR-1998; 98US-0079751.

(USSH) US DEPT HEALTH & HUMAN SERVICES.

PA Newton DL, Rybak SM;

PI MPI; 1999-610847/52.

DR N-PSDB; AA208128.

PT New recombinant ribonucleases, used for killing target cells, e.g. for treating cancers, viral infections or autoimmune diseases -

PS Claim 34; Page 60; 71pp; English.

CC The present sequence is a recombinant Rana pipiens ribonuclease (RAPLRI) protein with Glniser. Carboxy terminal end of recombinant RAPLRI has a covalently bound ligand binding moiety, which can be a IL2 antibody directed against CD22 on cancerous B cells or human chorionic


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XX AC AAY39400;
XX DT 01-DEC-1999 (first entry)
XX DE Recombinant frog Oncnase.
XX KM Ribonuclease; protein synthesis; inhibition; cancer; cytotoxic.
XX OS Rana pipiens.
XX PN MO9946389-A1.
XX PD 16-SEP-1999.
XX PF 11-MAR-1999; 99MO-US04252.
XX PR 11-MAR-1998; 98US-0077557.
XX PA (IMMU-) IMMUNOMEDICS INC.
XX PI Goldenberg DM, Hansen H, Leung S;
XX DR WPI: 1999-551416/46.
XX DR N-PSDB; AAZ19767.
XX PT A new recombinant Oncnase used to treat, e.g. colon cancer -
XX PS Example 1; Fig 1; 42pp; English.
XX
XX CC This sequence represents recombinant frog Oncnase. Oncnase has
XX CC ribonuclease and anti-tumour activity. The cDNA was produced via PCR
XX CC (using primers AAZ19768-219769) of two synthetic DNAs whose sequences
XX CC encoded most of the N-terminal or the C-terminal amino acids of mature
XX CC Oncnase. The two PCR products generated encoded either the N-terminal
XX CC 54 amino acids (minus the initial methionine) or the C-terminal 51 amino
XX CC acids, and were ligated in frame at an NruI site. The cDNA was then
XX CC subcloned into a vector e.g., pBluescript, where the AUG initiation
XX CC codon was ligated to the cDNA. After expression in E. coli, the
XX CC recombinant protein was purified. The initial N-formyl methionine was
XX CC cleaved off and the now N-terminal glutamate residue cyclised to form an
XX CC N-terminal pyroglutamate. The pyroglutamate residue forms part of the
XX CC phosphate binding pocket of Oncnase and is essential for both
XX CC ribonuclease and anti-tumour activity. Oncnase is a 12 kD ribonuclease
XX CC which causes cell death as a result of potent inhibition of protein
XX CC synthesis by a mechanism involving inactivation of cellular RNA. It is
XX CC not inhibited by mammalian placental ribonuclease inhibitor, which may
XX CC explain its enhanced cytotoxicity relative to mammalian enzymes. It has
XX CC anti-tumour activity against a variety of solid tumours e.g., colon or
XX CC pancreatic cancers, and can be used alone or in combination with other
XX CC anti-cancer agents such as tamoxifen. When used as an anti-tumour agent,
XX CC Oncnase can be conjugated to a marker which targets it to a specific
XX CC cell type.
XX
XX SQ Sequence 105 AA;
XX
XX Query Match 94.1%; Score 546; DB 20; Length 105;
XX Best Local Similarity 93.3%; Pred. No. 5.7e-59;
XX Matches 98; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
XX
XX QY 1 MODMLTFQKKHLTNTRDVCNNILSTNLFHCKDKNTFTYSRPPVKAICKGIIASKNVLT 60
XX DB 1 MQDWLTFQKKHITNTKDVCDDNIMSTNLFHCKDKNTFTYSRPPVKAICKGIIASKNVLT 60
XX QY 61 TSEFYISDCNVTSRPCKYKLLKXSTITFCVTCENQAPVHPFGVGH 105
XX DB 61 TSEFYISDCNVTSRPCKYKLLKXSTITFCVTCENQAPVHPFGVGS 105
XX
XX RESULT 11
XX ID AAW35125
XX AAW35125 standard; Protein; 355 AA.

```

```

AC AAW35125;
XX DT 20-APR-1998 (first entry)
XX DE R. pipiens recombinant RNase rOnc fusion protein 1.
XX KM RNase A; ribonuclease; cytotoxic; oncnase; nOnc; immunofusion;
XX OS Rana pipiens.
XX PN MO9731116-A2.
XX PD 28-AUG-1997.
XX PF 19-FEB-1997; 97MO-US02588.
XX PR 21-FEB-1996; 96US-0011800.
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX PI Boque L, Newton DL, Rybak SM, Wlodawer A;
XX DR WPI: 1997-435168/40.
XX DR N-PSDB; AAT94963.
XX PT Ribonuclease molecules based on native Oncnase - used for killing
XX PS cells, particularly tumour cells
XX PS Disclosure; Page 67; 90pp; English.
XX
XX CC Sequences AAW35125 to AAW35135 represent recombinant fusion proteins
XX CC (fOnc) which are modifications of the RNase Oncnase (rOnc). Such
XX CC novel ribonuclease molecules are highly cytotoxic and can be used alone
XX CC or to form chemical conjugates or to target recombinant immunofusions.
XX CC They are used particularly for decreasing tumour cell growth. They can
XX CC also be used for cell separation in vitro by selectively killing unwanted
XX CC types of cells, e.g. in bone marrow prior to transplantation into a
XX CC patient undergoing marrow ablation by radiation, or for killing leukemia
XX CC cells or T-cells that would cause graft versus host disease. The toxins
XX CC can also be used to selectively kill unwanted cells in culture. The new
XX CC ribonucleases have increased cytotoxic activity compared to nOnc and
XX CC also lower immunogenicity in humans.
XX
XX SQ Sequence 355 AA;
XX
XX Query Match 94.1%; Score 546; DB 18; Length 355;
XX Best Local Similarity 93.3%; Pred. No. 2.8e-57;
XX Matches 98; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
XX
XX QY 1 MODMLTFQKKHLTNTRDVCNNILSTNLFHCKDKNTFTYSRPPVKAICKGIIASKNVLT 60
XX DB 251 MEDMLTFQKKHITNTKDVCDDNIMSTNLFHCKDKNTFTYSRPPVKAICKGIIASKNVLT 310
XX QY 61 TSEFYISDCNVTSRPCKYKLLKXSTITFCVTCENQAPVHPFGVGH 105
XX DB 311 TSEFYISDCNVTSRPCKYKLLKXSTITFCVTCENQAPVHPFGVGS 355
XX
XX RESULT 12
XX ID AAW35130
XX AAW35130 standard; Protein; 358 AA.
XX
XX AC AAW35130;
XX DT 20-APR-1998 (first entry)
XX DE R. pipiens recombinant RNase rOnc fusion protein 6.
XX KM RNase A; ribonuclease; cytotoxic; oncnase; nOnc; immunofusion;
XX KW tumour cell growth; frog.
XX

```

```

OS Rana pipiens.
XX Synthetic.
XX
XX MO9731116-A2.
XX
XX 28-AUG-1997.
XX
XX 19-FEB-1997; 97WO-US02588.
XX
XX 21-FEB-1996; 96US-0011800.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Boque L, Newton DL, Rybak SM, Wlodawer A;
XX
XX WPI; 1997-435168/40.
XX
XX N-PSDB; AAT94968.
XX
XX Ribonuclease molecules based on native Onconase - used for killing
XX cells, particularly tumour cells
XX
XX
XX PS Disclosure; Page 72; 90pp; English.
XX
XX Sequences AAW35125 to AAW35135 represent recombinant fusion proteins
XX (rOnC) which are modifications of the RNase Onconase (RTM) (nOnC). Such
XX novel ribonuclease molecules are highly cytotoxic and can be used alone
XX or to form chemical conjugates or to target recombinant immunofusions.
XX They are used particularly for decreasing tumour cell growth. They can
XX also be used for cell separation in vitro by selectively killing unwanted
XX types of cells, e.g. in bone marrow prior to transplantation into a
XX patient undergoing marrow ablation by radiation, or for killing leukaemia
XX cells or T-cells that would cause graft versus host disease. The toxins
XX can also be used to selectively kill unwanted cells in culture. The new
XX ribonucleases have increased cytotoxic activity compared to nOnC and
XX also lower immunogenicity in humans.
XX
XX Sequence 358 AA:
XX
XX Query Match 94.1%; Score 546; DB 18; Length 358;
XX Best Local Similarity 93.3%; Pred. No. 2.8e-57;
XX Matches 98; Conservative 4; Mismatches 3; Indels 0; Gaps 0
XX
OY 1 MODWLTFFQKHLITNRDVCNNILSTNLFHCXDKNTFIYSRPPVKAICKGIASRNVLT 60
XX :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MEDWLTFFQKHLITNRDVCNNIMSTNLFHCXDKNTFIYSRPPVKAICKGIASRNVLT 60
XX TSEFLLSDCNVTSRCPCKYKLKKSTTFPCVTCGNOAPVHFGVGHG 105
XX TSEFLLSDCNVTSRCPCKYKLKKSTNKKFCVTCGNOAPVHFGVGS 105
XX
RESULT 13
AAW30301
XX AAW30301 standard; protein; 104 AA.
XX
XX AAW30301;
XX
XX AC
XX DT 09-JUN-1998 (first entry)
XX
XX DE
XX REcombinant onc protein.
XX
XX KM Onc; onconase; ribonuclease; frog; antitumour; pancreatic cancer;
XX KW human immunodeficiency virus type-1; HIV1; replication.
XX
XX OS Rana pipiens.
XX
XX PN MO9731112-A1.
XX
XX PD 16-OCT-1997.
XX
XX PF 04-APR-1997; 97WO-US05675.
XX
XX PR 04-APR-1996; 96US-0626288.
XX

```

XX	(USSH) US DEPT HEALTH & HUMAN SERVICES.
PA	
XX	Ardelt W, Boix E, Vasandani VM, Wu YN, Youle RJ;
PI	
XX	WPI; 1997-512725/47.
DR	
XX	
PT	Recombinant Onc protein with glutamine residue at position 1 -
XX	useful as antitumour and antiviral agent, also as cell culture
PT	selection agent
XX	
PS	Claim 1; Page 28; 35pp; English.
XX	
CC	This sequence represents a recombinant Onc protein comprising a 104 amino
CC	acid sequence having Gln at position 1. Onc, a ribonuclease from Rana
CC	pipiens oocytes, is known as an antitumour agent (e.g. for treating
CC	pancreatic cancer) and inhibitor of human immunodeficiency virus type-1
CC	replication. It can be used therapeutically or as a cell-culture
CC	inhibition agent, e.g. to identify gene therapy compositions able to
CC	inhibit tumour growth.
XX	
SQ	Sequence 104 AA;
Query Match	93.8%; Score 544; DB 18; Length 104;
Best Local Similarity	94.2%; Pred. No. 9.9e-58;
Matches 98; Conservative 3; Mismatches 3; Indels 0; Gaps 0;	
Dd	2 ODMLTPOKGLTNRDVDCNNILSTNLPHCKDKNTFTYSRPPVKATICKGIASKNVLT 61 1 QDMLTFQKHITNRDVDCCDNIMSTNLPHCKDKNTFTYSRPPVKATICKGIASKNVLT 60
Oy	62 SEFLSDCNVTSRPCKYKLKKSTITTCVCENQAPVHFVGVC 105 61 SEFLSDCNVTSRPCKYKLKKSTITTCVCENQAPVHFVGVC 104
Db	
RESULT 14	
AAB31666	
ID AAB31666 standard; protein; 104 AA.	
AC AAB31666;	
DT 30-APR-2001 (first entry)	
DE Amino acid sequence of a frog ribonuclease protein.	
KW Frog; ribonuclease; ranpirinase; RNase.	
OS Rana pipiens.	
XX	
FH Key Location/Qualifiers	
FT Modified-site 1 /note= "this Gln is autocyclised to pyroglutamic acid"	
XX	
FN US6175003-B1.	
PD 16-JAN-2001.	
PF 10-SEP-1999; 99US-0394268.	
PR 10-SEP-1999; 99US-0394268.	
PA (ALFA-) ALFACELP CORP.	
PI Saxena SK.	
WPI; 2001-167808/17.	
New nucleic acids encoding a ribonuclease (RNase), useful for the precise targeting of RNase to a predetermined cell receptor - Claim 1; Columns 5-6; 7pp; English.	

The present sequence represents a frog ribonuclease protein (ramprinaase) (Kraese). The specification describes a synthetic ribonuclease protein, in which the addition of cysteine in the ribonuclease facilitates the chemical linking of a targeting molecule by the single reactive sulfhydryl group. The specification also describes a method for the production of ramprinaase using DNA technology instead of processing biological material. The re-engineering of the protein molecule allows easier attachment to a targeting molecule thereby making it possible for the ribonuclease to be delivered to a particular cell receptor where it might be most effective.

SQ Sequence 104 AA;

Query Match	93.8%	Score 544;	DB 22;	Length 104;
Best Local Similarity	94.2%;	Pred. No. 9.9e-58;		
Matches 98;	Conservative 3;	Mismatches 3;	Indels 0;	Gaps 0;

```

Oy      2 QDWLTQKQKHLTNTRDVCNNIISTNLPHCKDKNFTIYSRPEPVAKICKGIASKNVLT 61
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1 QDWLTQKQKHLTNTRDVCNNIISTNLPHCKDKNFTIYSRPEPVAKICKGIASKNVLT 60

```

```
Oy      62 SEFYLSDCNVTSRPCCKYKLLKSTITFCVTCENQAPVHFVGVC 105
        |||||
Db       61 SEFYLSDCNVTSRPCCKYKLLKSTNKFCVTCENQAPVHFGVGC 104
```

RESULT 15

ID ABG32650 standard; Protein; 104 AA.

AC ABG32650 ;

DT 15-NOV-2002 (first entry)

DE Northern leopard frog ranpirinase protein.

KW Northern leopard frog; ranpirnase; site-directed mutation; ribonuclease.

OS Rana pipiens.

PN US6423515-B1.

PD 23-JUL-2002.
YX

PF 14-OCT-2000; 2000US-0687748.
YY

PR 10-SEP-1999; 99US-0394268.
YY

PA (ALFA-) ALFACELL CORP.
XXPI Saxena SK;
XX

DR WPI; 2002-664633/71.
XX

PT Constructing recombinant plasmid DNA to different site-directed mutations to produce nucleic acid, using different polymerase chain reaction protocols -

PS Claim 1; Column 5-6; 8pp; English.

The present invention relates to a new method of constructing isolated nucleic acid encoding ribonuclease protein with N-terminal Met at position -1 and Glu at position 1, where its Met has been cleaved and its Glu has been autocyclised. The method of the invention involves subcloning pEHD-ronc(01.M23), plasmid DNA to two different site-directed mutations, each using overlapping PCR protocol. The method is useful for constructing an isolated nucleic acid encoding the ribonuclease. The present amino acid sequence represents the northern leopard frog rarnpinase protein of the invention.

SQ Sequence 104 AA;

Query Match	93.8%	Score 544;	DB 23;	Length 104;
Best Local Similarity	94.2%	Pred. No. 9.9e-58;		
Matches 98;	Conservative 3;	Mismatches 3;	Indels 0;	Gaps 0;

```

Oy 2 QDMLTFQKKLITNTRVDCCNNLSTNLPHCKDKNTFIYSRPEPKAICKGIASKVLT 61
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 QDMLTFQKKHITNTRVDCCDNIWSTNLPHCKDKNTFIYSRPEPKAICKGIASKVLT 60

```

```

Qy      62 SEFYLSDCNVTSRPCKYKYLKKSTITFCVTCENQAPVHVFVGHC 105
        |||||
Db      61 SEFYLSDCNVTSRPCKYKYLKKSTNKFVTCENQAPVHVFVGSC 104

```

Search completed: January 22, 2004, 12:06:23
Job time : 33.0337 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 22, 2004, 12:01:30 : Search time 12.5843 Seconds
(without alignments)
353.031 Million cell updates/sec

Title: US-09-622-613C-8

Perfect score: 580

Sequence: 1 MODULFQKXHLNTRDVC.....TECVTCENQAPVHFVGVGHC 105

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/prodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/prodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/prodata/1/iaa/5A_COMB.pep:*
4: /cgn2_6/prodata/1/iaa/5B_COMB.pep:*
5: /cgn2_6/prodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/prodata/1/iaa/backfill1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	546	94.1	104	1	US-08-467-955-2
2	546	94.1	105	3	US-08-875-811-39
3	546	94.1	355	3	US-08-875-811-41
4	546	94.1	358	3	US-08-875-811-51
5	544	93.8	104	4	US-09-394-268-1
6	544	93.8	104	4	US-09-687-748-1
7	544	93.8	112	3	US-08-875-811-32
8	544	93.8	129	3	US-08-875-811-63
9	544	93.8	251	3	US-08-875-811-59
10	544	93.8	254	3	US-08-875-811-61
11	544	93.8	355	3	US-08-875-811-49
12	544	93.8	355	3	US-08-875-811-57
13	544	93.8	355	3	US-08-875-811-64
14	544	93.8	366	3	US-08-875-811-55
15	544	93.8	379	3	US-08-875-811-43
16	541	93.3	104	1	US-08-283-971-1
17	541	93.3	104	1	US-07-921-619-1
18	541	93.3	104	1	US-08-467-955-1
19	541	93.3	104	2	US-08-891-268-13
20	541	93.3	104	3	US-09-394-268-2
21	541	93.3	104	4	US-09-687-748-2
22	539	92.9	104	4	US-08-875-811-1
23	539	92.9	104	4	US-09-071-672-1
24	539	92.9	105	3	US-08-875-811-26
25	539	92.9	106	3	US-08-875-811-28
26	539	92.9	107	3	US-08-875-811-30
27	538	92.8	105	3	US-08-875-811-24

28	535	92.2	358	3	US-08-875-811-45	Sequence 45, Appl
29	535	92.2	365	3	US-08-875-811-53	Sequence 53, Appl
30	516	89.0	107	3	US-08-875-811-20	Sequence 20, Appl
31	483	83.3	360	3	US-08-875-811-47	Sequence 47, Appl
32	471.5	81.3	111	3	US-08-875-811-22	Sequence 22, Appl
33	433	74.7	83	3	US-08-875-811-2	Sequence 2, Appl1
34	433	74.7	83	4	US-09-071-672-3	Sequence 3, Appl1
35	277	47.8	111	3	US-08-891-848-12	Sequence 12, Appl
36	277	47.8	111	3	US-08-875-811-8	Sequence 8, Appl1
37	205.5	35.4	114	3	US-09-223-118-4	Sequence 4, Appl1
38	193.5	33.4	114	3	US-09-223-118-2	Sequence 2, Appl1
39	192.5	33.2	114	3	US-09-223-118-1	Sequence 1, Appl1
40	190.5	32.8	114	3	US-09-223-118-3	Sequence 3, Appl1
41	152.5	26.3	169	1	US-08-441-629-2	Sequence 2, Appl1
42	152.5	26.3	169	3	US-08-776-207-2	Sequence 2, Appl1
43	152.5	26.3	169	4	US-09-507-773-2	Sequence 2, Appl1
44	152.5	26.3	169	5	PCT-US95-09172-2	Sequence 2, Appl1
45	143	24.7	28	3	US-08-875-811-3	Sequence 3, Appl1

ALIGNMENTS

RESULT 1
US-08-467-955-2
Sequence 2, Application US/08467955
Patent No. 572805
GENERAL INFORMATION:
APPLICANT: Ardelt Ph.D, Wojciech J.
TITLE OF INVENTION: PHARMACEUTICALS AND METHOD FOR MAKING THEM
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSER: Mark H. Jay, P.A.
STREET: P.O. Box E
CITY: Short Hills
STATE: New Jersey
COUNTRY: USA
ZIP: 07078-0383
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,955
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/178,118
FILING DATE: 06-APR-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/436,141
FILING DATE: 13-NOV-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/814,332
FILING DATE: 03-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/283,970
FILING DATE: 01-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Jay, Mark H.
REGISTRATION NUMBER: 27507
REFERENCE/DOCKET NUMBER: 5007 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-912-9066
TELEFAX: 201-912-0442
TELEX: No. 572805 Applicablc
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 104 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: protein
HYPOTHETICAL: N
ANTI-SENSE: N
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Rana pipiens
DEVELOPMENTAL STAGE: Oocyte
US-08-467-955-2

Query Match 94.1%; Score 546; DB 1; Length 104;
Best Local Similarity 94.2%; Pred. No. 8.7e-60;
Matches 98; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 QDWLTFQKXHLINTRDVDCNNILSTNLFHCKDKNTFIYSRPPVYAKICKGIISKVLT 61
Db 1 EDWLTFOKXHLINTRDVDCNNIMSTNLFHCKDKNTFIYSRPPVYAKICKGIISKVLT 60
QY 62 TSEFYSDCNVTSRPPCKYKLLKSTITFCVTCENQAPVHFVGVGHC 105
Db 61 TSEFYSDCNVTSRPPCKYKLLKSTITFCVTCENQAPVHFVGVGHC 104

RESULT 2
US-08-875-811-39

Sequence 39; Application US/08875811
Patent No. 6045793
GENERAL INFORMATION:
APPLICANT: Rydak, Sueanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Bogue, Lluís
APPLICANT: Wlodawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Paris, Susan K.
REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 015280-244100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 105 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-875-811-39

Query Match 94.1%; Score 546; DB 3; Length 105;
Best Local Similarity 93.3%; Pred. No. 8.8e-60;
Matches 98; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 MODWLTFOKXHLINTRDVDCNNILSTNLFHCKDKNTFIYSRPPVYAKICKGIISKVLT 60
Db 1 MEDWLTFOKXHLINTRDVDCNNIMSTNLFHCKDKNTFIYSRPPVYAKICKGIISKVLT 60
QY 61 TSEFYSDCNVTSRPPCKYKLLKSTITFCVTCENQAPVHFVGVGHC 105
Db 61 TSEFYSDCNVTSRPPCKYKLLKSTITFCVTCENQAPVHFVGVGHC 105

RESULT 3
US-08-875-811-41

Sequence 41; Application US/08875811
Patent No. 6045793
GENERAL INFORMATION:
APPLICANT: Rydak, Sueanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Bogue, Lluís
APPLICANT: Wlodawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Paris, Susan K.
REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 015280-244100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-875-811-41

Query Match 94.1%; Score 546; DB 3; Length 355;
Best Local Similarity 93.3%; Pred. No. 4.4e-59;
Matches 98; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 MODWLTFOKXHLINTRDVDCNNILSTNLFHCKDKNTFIYSRPPVYAKICKGIISKVLT 60
Db 251 MEDWLTFOKXHLINTRDVDCNNIMSTNLFHCKDKNTFIYSRPPVYAKICKGIISKVLT 310
QY 61 TSEFYSDCNVTSRPPCKYKLLKSTITFCVTCENQAPVHFVGVGHC 105
Db 311 TSEFYSDCNVTSRPPCKYKLLKSTITFCVTCENQAPVHFVGVGHC 355

RESULT 4
US-08-875-811-51

Sequence 51, Application US/08875811
Patent No. 6045793
GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Boque, Luis
APPLICANT: Mlodawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Paris, Susan K.
REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 015280-244100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 358 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-875-811-51

Query Match 94.1%; Score 546; DB 3; Length 358;
Best Local Similarity 93.3%; Pred. No. 4.4e-59;
Matches 98; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 MODMLTFQKHLITNTRDVCNNILSTNLFHCKDKNTFIYSRPEPVKAIKGIISKVLT 60
DB 1 MEDMLTFQKHLITNTRDVCNNIMSTNLFHCKDKNTFIYSRPEPVKAIKGIISKVLT 60

QY 61 TSEFYISDCNVTSRPCKYKLLKSKSTTTCVTCENQAPVHFGVGC 105
DB 61 TSEFYISDCNVTSRPCKYKLLKSKSTNKFCTCENQAPVHFGVGC 105

RESULT 5
US-09-394-268-1
Sequence 1, Application US/09394268
Patent No. 6175003
GENERAL INFORMATION:
APPLICANT: Saxena, Shalendra K
APPLICANT: Mlodawer, Alexander
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING RIBONUCLEASES AND METHODS OF
FILE REFERENCE: 5013
CURRENT APPLICATION NUMBER: US/09/394,268
CURRENT FILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1

LENGTH: 104
TYPE: PRT
ORGANISM: Rana pipiens
US-09-394-268-1

Query Match 93.8%; Score 544; DB 3; Length 104;
Best Local Similarity 94.2%; Pred. No. 1.5e-59;
Matches 98; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 QDWLTFQKHLITNTRDVCNNILSTNLFHCKDKNTFIYSRPEPVKAIKGIISKVLT 61
DB 1 QDWLTFQKHLITNTRDVCNNIMSTNLFHCKDKNTFIYSRPEPVKAIKGIISKVLT 60

QY 62 SEFYISDCNVTSRPCKYKLLKSKSTTTCVTCENQAPVHFGVGC 105
DB 61 SEFYISDCNVTSRPCKYKLLKSKSTNKFCTCENQAPVHFGVGC 104

RESULT 6
US-09-687-748-1
Sequence 1, Application US/09687748
Patent No. 6423515
GENERAL INFORMATION:
APPLICANT: Saxena, Shalendra K
TITLE OF INVENTION: METHODS OF MAKING NUCLEIC ACIDS ENCODING RIBONUCLEASES
FILE REFERENCE: 5013 US 01
CURRENT APPLICATION NUMBER: US/09/687,748
CURRENT FILING DATE: 2000-10-14
PRIOR APPLICATION NUMBER: 09/394,268
PRIOR FILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 104
TYPE: PRT
ORGANISM: Rana pipiens
US-09-687-748-1

Query Match 93.8%; Score 544; DB 4; Length 104;
Best Local Similarity 94.2%; Pred. No. 1.5e-59;
Matches 98; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 QDWLTFQKHLITNTRDVCNNILSTNLFHCKDKNTFIYSRPEPVKAIKGIISKVLT 61
DB 1 QDWLTFQKHLITNTRDVCNNIMSTNLFHCKDKNTFIYSRPEPVKAIKGIISKVLT 60

QY 62 SEFYISDCNVTSRPCKYKLLKSKSTTTCVTCENQAPVHFGVGC 105
DB 61 SEFYISDCNVTSRPCKYKLLKSKSTNKFCTCENQAPVHFGVGC 104

RESULT 7
US-08-875-811-32
Sequence 32, Application US/08875811
Patent No. 6045793
GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Boque, Luis
APPLICANT: Mlodawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Paris, Susan K.
REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 015280-244100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-875-811-32

Query Match 93.8%; Score 544; DB 3; Length 112;
Best Local Similarity 93.3%; Pred. No. 1,7e-59;
Matches 98; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 MODLTFQKKHITNTRDVDCNNILSTNLFHCKDKNTFYISRPVPVKAICKGIASKNVLT 60
DB 8 MSMDLTFQKKHITNTRDVDCNNILSTNLFHCKDKNTFYISRPVPVKAICKGIASKNVLT 67
QY 61 TSEFYLSDCNVTSPRCCKYKLKSKSTTTCVTCENQAPVHFVGVC 105
DB 68 TSEFYLSDCNVTSPRCCKYKLKSKSTNKCVCENQAPVHFVGVC 112

RESULT 8
US-08-875-811-63
Sequence 63, Application US/08875811
Patent No. 6045793
GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Bogue, Luuis
APPLICANT: Wlodawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:

NAME: Paris, Susan K.
REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 015280-244100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 129 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-875-811-63

Query Match 93.8%; Score 544; DB 3; Length 129;
Best Local Similarity 94.2%; Pred. No. 2e-59;
Matches 98; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 QDWLTFQKKHITNTRDVDCNNILSTNLFHCKDKNTFYISRPVPVKAICKGIASKNVLT 61
DB 26 QDWLTFQKKHITNTRDVDCNNILSTNLFHCKDKNTFYISRPVPVKAICKGIASKNVLT 85
QY 62 SEFYLSDCNVTSPRCCKYKLKSKSTTTCVTCENQAPVHFVGVC 105
DB 86 SEFYLSDCNVTSPRCCKYKLKSKSTNKCVCENQAPVHFVGVC 129

RESULT 9
US-08-875-811-59
Sequence 59, Application US/08875811
Patent No. 6045793
GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Bogue, Luuis
APPLICANT: Wlodawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Paris, Susan K.
REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 015280-244100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 251 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-875-811-59

Query Match 93.8%; Score 544; DB 3; Length 251;
Best Local Similarity 93.3%; Pred. No. 4.9e-59;
Matches 98; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MODWLTFOKKHLLTNRDVCNNILSTNLFHCKDKNTFYISREPPVKAICKGIIASKNVLT 60
Db 147 MSDWLTFOKKHLLTNRDVCNNILSTNLFHCKDKNTFYISREPPVKAICKGIIASKNVLT 206

Qy 61 TSEFYISDCNVTSRPCKYKLLKSKSTTFCVTCENQAPVHFVGVC 105
Db 207 TSEFYISDCNVTSRPCKYKLLKSKSTTFCVTCENQAPVHFVGVC 251

RESULT 10

US-08-875-811-61
; Sequence 61, Application US/08875811
; Patent No. 6045793
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Boque, Lluís
; APPLICANT: Wlodawer, Alexander
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,811
; FILING DATE: 19-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/02588
; FILING DATE: 19-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/011,800
; FILING DATE: 21-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Faris, Susan K.
; REGISTRATION NUMBER: 41,739
; REFERENCE/DOCKET NUMBER: 015280-244100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 61:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 254 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-875-811-61

Query Match 93.8%; Score 544; DB 3; Length 254;
Best Local Similarity 93.3%; Pred. No. 5e-59;
Matches 98; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MODWLTFOKKHLLTNRDVCNNILSTNLFHCKDKNTFYISREPPVKAICKGIIASKNVLT 60
Db 1 MSDWLTFOKKHLLTNRDVCNNILSTNLFHCKDKNTFYISREPPVKAICKGIIASKNVLT 60
Qy 61 TSEFYISDCNVTSRPCKYKLLKSKSTTFCVTCENQAPVHFVGVC 105

Db 61 TSEFYISDCNVTSRPCKYKLLKSKSTTFCVTCENQAPVHFVGVC 105

RESULT 11

US-08-875-811-49
; Sequence 49, Application US/08875811
; Patent No. 6045793
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Boque, Lluís
; APPLICANT: Wlodawer, Alexander
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,811
; FILING DATE: 19-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/02588
; FILING DATE: 19-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/011,800
; FILING DATE: 21-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Faris, Susan K.
; REGISTRATION NUMBER: 41,739
; REFERENCE/DOCKET NUMBER: 015280-244100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-875-811-49

Query Match 93.8%; Score 544; DB 3; Length 355;
Best Local Similarity 93.3%; Pred. No. 7.7e-59;
Matches 98; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MODWLTFOKKHLLTNRDVCNNILSTNLFHCKDKNTFYISREPPVKAICKGIIASKNVLT 60
Db 251 MSDWLTFOKKHLLTNRDVCNNILSTNLFHCKDKNTFYISREPPVKAICKGIIASKNVLT 310
Qy 61 TSEFYISDCNVTSRPCKYKLLKSKSTTFCVTCENQAPVHFVGVC 105
Db 311 TSEFYISDCNVTSRPCKYKLLKSKSTTFCVTCENQAPVHFVGVC 355

RESULT 12

US-08-875-811-57
; Sequence 57, Application US/08875811
; Patent No. 6045793
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Boque, Lluís
; APPLICANT: Wlodawer, Alexander

TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Faris, Susan K.
REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 015280-244100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-875-811-57

Query Match 93.8%; Score 544; DB 3; Length 355;
Best Local Similarity 93.3%; Pred. No. 7,7e-59;
Matches 98; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 MODLTFQKKHLNTFDVDCNNLSTNLFPHCKDKNTFTYSRPPVPAICKGIITASKVLT 60
DB 1 MSWMLTFQKKHITNTDVCDDNIMSTNLFPHCKDKNTFTYSRPPVPAICKGIITASKVLT 60

QY 61 TSEFYLSDCNVTSRPCKYKLLKSTITFCVTCENQAPVHFVGVGHC 105
DB 61 TSEFYLSDCNVTSRPCKYKLLKSTINKFCVTCENQAPVHFVGVGSC 105

RESULT 13
US-08-875-811-64
Sequence 64, Application US/08875811
Patent No. 6045793
GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Bogue, Lluís
APPLICANT: Mlodawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Faris, Susan K.
REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 015280-244100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 64:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..355
OTHER INFORMATION: /note="E6FB[Met-(-1)]Seronc"
US-08-875-811-64

Query Match 93.8%; Score 544; DB 3; Length 355;
Best Local Similarity 93.3%; Pred. No. 7,7e-59;
Matches 98; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 MODLTFQKKHLNTFDVDCNNLSTNLFPHCKDKNTFTYSRPPVPAICKGIITASKVLT 60
DB 251 MSWMLTFQKKHITNTDVCDDNIMSTNLFPHCKDKNTFTYSRPPVPAICKGIITASKVLT 310

QY 61 TSEFYLSDCNVTSRPCKYKLLKSTITFCVTCENQAPVHFVGVGHC 105
DB 311 TSEFYLSDCNVTSRPCKYKLLKSTINKFCVTCENQAPVHFVGVGSC 355

RESULT 14
US-08-875-811-55
Sequence 55, Application US/08875811
Patent No. 6045793
GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Bogue, Lluís
APPLICANT: Mlodawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Paris, Susan K.
REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 015280-244100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 366 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-875-811-55

Query Match 93.8%; Score 544; DB 3; Length 366;
Best Local Similarity 93.3%; Pred. No. 8.1e-59;
Matches 98; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MODWLTFOKQHLINTRDVDCNNILSTNLFHCKDKNTFIYSRPEPVKAICKGIASKNVLT 60
Db 262 MSDWLTFOKQHLINTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIASKNVLT 321
Qy 61 TSEFYLSDCNVTSRPPCKYKLLKSTITFCVTCENQAPVHFVGVGHC 105
Db 322 TSEFYLSDCNVTSRPPCKYKLLKSTINKFCVTCENQAPVHFVGVGSC 366

RESULT 15
US-08-875-811-43
Sequence 43, Application US/08875811
Patent No. 6045793
GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: Bogue, Louis
APPLICANT: Wlodawer, Alexander
TITLE OF INVENTION: Recombinant Ribonuclease Proteins
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,811
FILING DATE: 19-FEB-1998
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/02588
FILING DATE: 19-FEB-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/011,800
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Paris, Susan K.
REGISTRATION NUMBER: 41,739
REFERENCE/DOCKET NUMBER: 015280-244100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 379 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-875-811-43

Query Match 93.8%; Score 544; DB 3; Length 379;
Best Local Similarity 94.2%; Pred. No. 8.4e-59;
Matches 98; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 2 ODWLTFOKQHLINTRDVDCNNILSTNLFHCKDKNTFIYSRPEPVKAICKGIASKNVLT 61
Db 26 QDWLTFOKQHLINTRDVDCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIASKNVLT 85
Qy 62 SEFYLSDCNVTSRPPCKYKLLKSTITFCVTCENQAPVHFVGVGHC 105
Db 86 SEFYLSDCNVTSRPPCKYKLLKSTINKFCVTCENQAPVHFVGVGSC 129

Search completed: January 22, 2004, 12:10:06
Job time : 12.5843 secs

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OM protein - protein search, using sw model

Run on: January 22, 2004, 12:02:15 ; Search time 24.9719 Seconds
(without alignments)
869.271 Million cell updates/sec

Title: US-09-622-613C-8

Perfect score: 580

Sequence: 1 MODWLTFOKKHLTNTRDVDC.....TFCVTGQNPVHFGVGHHC 105

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 777136 seqs, 206736638 residues

Total number of hits satisfying chosen parameters: 777136

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUBCOMB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	574	99.0	105	US-09-948-391A-8
2	574	99.0	111	US-09-948-391A-9
3	573	99.8	111	US-09-961-400-9
4	571	99.4	105	US-09-948-391A-6
5	571	99.4	105	US-09-961-400-6
6	566	97.6	104	US-09-961-400-2
7	566	97.6	105	US-09-948-391A-13
8	566	97.6	105	US-09-961-400-13
9	566	97.6	105	US-09-948-391A-28
10	566	97.6	127	US-09-961-400-28
11	563	97.1	105	US-09-948-391A-4
12	562	96.9	104	US-09-961-400-4
13	562	96.9	104	US-09-948-391A-11
14	561	96.7	104	US-09-961-400-11
15	561	96.7	104	US-09-961-400-11

16	557	96.0	104	US-09-948-391A-2	Sequence 2, Appli
17	549	94.7	105	US-10-153-882-2	Sequence 2, Appli
18	539	92.9	104	US-09-986-119-1	Sequence 1, Appli
19	539	92.9	104	US-09-918-887-1	Sequence 1, Appli
20	433	74.7	83	US-09-986-119-3	Sequence 3, Appli
21	433	74.7	83	US-09-918-887-3	Sequence 3, Appli
22	275.5	47.5	111	US-09-948-391A-21	Sequence 21, Appli
23	275.5	47.5	111	US-09-961-400-21	Sequence 21, Appli
24	275.5	47.5	117	US-09-948-391A-22	Sequence 22, Appli
25	275.5	47.5	117	US-09-961-400-22	Sequence 22, Appli
26	274.5	47.3	111	US-09-961-400-17	Sequence 17, Appli
27	270.5	46.6	110	US-09-961-400-19	Sequence 19, Appli
28	269.5	46.5	110	US-09-948-391A-15	Sequence 15, Appli
29	269.5	46.5	111	US-09-961-400-15	Sequence 15, Appli
30	269.5	46.5	111	US-09-948-391A-26	Sequence 26, Appli
31	269.5	46.5	111	US-09-961-400-26	Sequence 26, Appli
32	268.5	46.3	111	US-09-948-391A-17	Sequence 17, Appli
33	264.5	45.6	110	US-09-948-391A-19	Sequence 19, Appli
34	264.5	45.6	110	US-09-948-391A-24	Sequence 24, Appli
35	264.5	45.6	110	US-09-961-400-24	Sequence 24, Appli
36	152.5	26.3	169	US-10-016-447-2	Sequence 2, Appli
37	143	24.7	119	US-10-074-978A-139	Sequence 139, App
38	122.5	21.1	124	US-10-016-447-5	Sequence 5, Appli
39	109	18.8	147	US-09-286-240-6	Sequence 6, Appli
40	109	18.8	147	US-09-863-777-2	Sequence 2, Appli
41	109	18.8	147	US-09-731-872-254	Sequence 254, App
42	109	18.8	147	US-09-876-997-254	Sequence 254, App
43	106	18.3	124	US-09-981-286A-8	Sequence 8, Appli
44	100.5	17.3	99	US-10-074-978A-141	Sequence 141, App
45	98.5	17.0	89	US-10-074-978A-143	Sequence 143, App

ALIGNMENTS

RESULT 1

US-09-948-391A-8

Sequence 8, Application US/09948391A

Publication No. US20030027311A1

GENERAL INFORMATION:

APPLICANT: Rybak, Susanna M.

APPLICANT: Newton, Diane L.

APPLICANT: The United States of America

APPLICANT: as represented by The Secretary of the

APPLICANT: Department of Health and Human Services

TITLE OF INVENTION: Recombinant Anti-Tumor RNase

FILE REFERENCE: 015280-343110US

CURRENT APPLICATION NUMBER: US/09/948.391A

CURRENT FILING DATE: 2002-05-10

PRIOR APPLICATION NUMBER: US 60/079,751

PRIOR FILING DATE: 1998-03-27

PRIOR APPLICATION NUMBER: WO PCT/US99/06641

PRIOR FILING DATE: 1999-03-26

PRIOR APPLICATION NUMBER: US 09/622,613

PRIOR FILING DATE: 2000-08-17

NUMBER OF SEQ ID NOS: 43

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 8

LENGTH: 105

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Rana pipiens

OTHER INFORMATION: ribonuclease with Met at position 1 and Met24Leu

OTHER INFORMATION: substitution (recombinant Met(-1) RapiR1 Met23Leu)

US-09-948-391A-8

Query Match 99.0% Score 574; DB 11; Length 105;

Best Local Similarity 99.0% Pred No. 3e-56; 1; Indels 0; Gaps 0;

Matches 104; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MODWLTFOKKHLTNTRDVDCNNIISTNLPHCKDKNTFTYSRPPYKATCKGIASKNVLT 60

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Db      1  MODWLTFOKKHLTNRDVCNNILSTNLFHCKDKDNTFIYSRPEPVKAICKGIIASKNVLT 60
Qy      61  TSEFYLSDCNVTSRPCKYKLLKXSTITFCVTCENQAPVHFVGVGHC 105
Db      61  TSEFYLSDCNVTSRPCKYKLLKXSTITFCVTCENQAPVHFVGVGHC 105

RESULT 2
US-09-948-391A-9
; Sequence 9, Application US/09948391A
; Publication No. US20030027311A1
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: The United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Recombinant Anti-Tumor RNase
; FILE REFERENCE: 015280-343110US
; CURRENT APPLICATION NUMBER: US/09/948, 391A
; CURRENT FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 60/079, 751
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/622, 613
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Rana pipiens
; OTHER INFORMATION: ribonuclease with (His)6 tag, Met at position 7
; OTHER INFORMATION: and Met30Leu substitution (recombinant Met(-1))
; OTHER INFORMATION: RapLR1 Met23Leu-(His)6)
US-09-948-391A-9

Query Match          99.0%; Score 574; DB 11; Length 111;
Best Local Similarity 99.0%; Pred. No. 3.2e-58;
Matches 104; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1  MODWLTFOKKHLTNRDVCNNILSTNLFHCKDKDNTFIYSRPEPVKAICKGIIASKNVLT 60
Db      7  MODWLTFOKKHLTNRDVCNNILSTNLFHCKDKDNTFIYSRPEPVKAICKGIIASKNVLT 66
Qy      61  TSEFYLSDCNVTSRPCKYKLLKXSTITFCVTCENQAPVHFVGVGHC 105
Db      67  TSEFYLSDCNVTSRPCKYKLLKXSTITFCVTCENQAPVHFVGVGHC 111

RESULT 3
US-09-961-400-9
; Sequence 9, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: GOLDENBERG, DAVID M.
; APPLICANT: NEWTON, DIANNE L.
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 018733/1059
; CURRENT APPLICATION NUMBER: US/09/961, 400
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 09/622, 613
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/079, 751
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 43
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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Rana pipiens
US-09-961-400-9

Query Match          98.4%; Score 573; DB 11; Length 111;
Best Local Similarity 99.0%; Pred. No. 4.2e-58;
Matches 104; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1  MODWLTFOKKHLTNRDVCNNILSTNLFHCKDKDNTFIYSRPEPVKAICKGIIASKNVLT 60
Db      7  MODWLTFOKKHLTNRDVCNNILSTNLFHCKDKDNTFIYSRPEPVKAICKGIIASKNVLT 66
Qy      61  TSEFYLSDCNVTSRPCKYKLLKXSTITFCVTCENQAPVHFVGVGHC 105
Db      67  TSEFYLSDCNVTSRPCKYKLLKXSTNTFCVTCENQAPVHFVGVGHC 111

RESULT 4
US-09-948-391A-6
; Sequence 6, Application US/09948391A
; Publication No. US20030027311A1
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: The United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Recombinant Anti-Tumor RNase
; FILE REFERENCE: 015280-343110US
; CURRENT APPLICATION NUMBER: US/09/948, 391A
; CURRENT FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 60/079, 751
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/622, 613
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Rana pipiens
; OTHER INFORMATION: ribonuclease with Met at position 1 (recombinant
; OTHER INFORMATION: Met(-1) RapLR1)
US-09-948-391A-6

Query Match          98.4%; Score 571; DB 11; Length 105;
Best Local Similarity 98.1%; Pred. No. 6.7e-58;
Matches 103; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1  MODWLTFOKKHLTNRDVCNNILSTNLFHCKDKDNTFIYSRPEPVKAICKGIIASKNVLT 60
Db      1  MODWLTFOKKHLTNRDVCNNIMSTNLFHCKDKDNTFIYSRPEPVKAICKGIIASKNVLT 60
Qy      61  TSEFYLSDCNVTSRPCKYKLLKXSTITFCVTCENQAPVHFVGVGHC 105
Db      61  TSEFYLSDCNVTSRPCKYKLLKXSTNTFCVTCENQAPVHFVGVGHC 105

RESULT 5
US-09-961-400-6
; Sequence 6, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: GOLDENBERG, DAVID M.
; APPLICANT: NEWTON, DIANNE L.
```

```

; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
; FILE REFERENCE: 018733/1059
; CURRENT APPLICATION NUMBER: US/09/961,400
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 09/622,613
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/079,751
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Rana pipiens
US-09-961-400-6

Query Match          98.4%; Score 571; DB 11; Length 105;
Best Local Similarity 98.1%; Pred. No. 6.7e-58;
Matches 103; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDWLTFQKKHLTNRDVCNNILSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT 60
DB 1 MDWLTFQKKHLTNRDVCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT 60
QY 61 TSEFYLSDCNVTSRPCKYKLLKXSTITFCVTCENQAPVHFVGVGHC 105
DB 61 TSEFYLSDCNVTSRPCKYKLLKXSTITFCVTCENQAPVHFVGVGHC 105

RESULT 6
US-09-961-400-2
; Sequence 2, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: GOLDENBERG, DAVID M.
; APPLICANT: NEWTON, DIANNE L.
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 018733/1059
; CURRENT APPLICATION NUMBER: US/09/961,400
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 09/622,613
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/079,751
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 104
; TYPE: PRT
; ORGANISM: Rana pipiens
US-09-961-400-2

Query Match          97.6%; Score 566; DB 11; Length 104;
Best Local Similarity 98.1%; Pred. No. 2.5e-57;
Matches 102; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QDWLTFQKKHLTNRDVCNNILSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT 61
DB 1 QDWLTFQKKHLTNRDVCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT 60
QY 62 SEFYLSDCNVTSRPCKYKLLKXSTITFCVTCENQAPVHFVGVGHC 105
DB 61 SEFYLSDCNVTSRPCKYKLLKXSTITFCVTCENQAPVHFVGVGHC 104

RESULT 7
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US-09-948-391A-13
; Sequence 13, Application US/09948391A
; Publication No. US20030027311A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: NEWTON, DIANNE L.
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Recombinant Anti-Tumor RNase
; FILE REFERENCE: 015280-343110US
; CURRENT APPLICATION NUMBER: US/09/948,391A
; CURRENT FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 60/079,751
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/622,613
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Rana pipiens
; OTHER INFORMATION: ribonuclease with Met at position 1 and Gln2Ser
; OTHER INFORMATION: substitution (recombinant Met(-1) RnPLR1 Q1S)
US-09-948-391A-13

Query Match          97.6%; Score 566; DB 11; Length 105;
Best Local Similarity 97.1%; Pred. No. 2.5e-57;
Matches 102; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MDWLTFQKKHLTNRDVCNNILSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT 60
DB 1 MSDWLTFQKKHLTNRDVCNNIMSTNLFHCKDKNTFIYSRPEPVKAICKGIIASKNVLT 60
QY 61 TSEFYLSDCNVTSRPCKYKLLKXSTITFCVTCENQAPVHFVGVGHC 105
DB 61 TSEFYLSDCNVTSRPCKYKLLKXSTITFCVTCENQAPVHFVGVGHC 105

RESULT 8
US-09-961-400-13
; Sequence 13, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: GOLDENBERG, DAVID M.
; APPLICANT: NEWTON, DIANNE L.
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 018733/1059
; CURRENT APPLICATION NUMBER: US/09/961,400
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 09/622,613
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/079,751
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Rana pipiens
US-09-961-400-13

Query Match          97.6%; Score 566; DB 11; Length 105;
Best Local Similarity 97.1%; Pred. No. 2.5e-57;
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/ FILE REFERENCE: 015280-343110US
/ CURRENT APPLICATION NUMBER: US/09/948,391A
/ CURRENT FILING DATE: 2002-05-10
/ PRIOR APPLICATION NUMBER: US 60/079,751
/ PRIOR FILING DATE: 1998-03-27
/ PRIOR APPLICATION NUMBER: WO PCT/US99/06641
/ PRIOR FILING DATE: 1999-03-26
/ PRIOR APPLICATION NUMBER: US 09/622,613
/ PRIOR FILING DATE: 2000-08-17
/ NUMBER OF SEQ ID NOS: 43
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 4
/ LENGTH: 104
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:Rana pipiens
/ OTHER INFORMATION: ribonuclease with Met23Ileu substitution
/ OTHER INFORMATION: (recombinant RapLRI Met23Ileu)
US-09-948-391A-4
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Query Match          96.9%; Score 562; DB 11; Length 104;
Best Local Similarity 98.1%; Pred. No. 7,1e-57;
Matches 102; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Qy 2 QDMLTFQKHLLNTRDVDCNNILSTNLFPHCKDKNTFIYSRPEPVKAICKGIISKVLT 61
Db 1 QDMLTFQKHLLNTRDVDCNNILSTNLFPHCKDKNTFIYSRPEPVKAICKGIISKVLT 60

Qy 62 SEFYISDCNVTSRPCKYKLLKKSSTTFCTVCENQAPVHFVGHC 105
Db 61 FEFYISDCNVTSRPCKYKLLKKSSTTFCTVCENQAPVHFVGHC 104
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RESULT 13
US-09-961-400-4
/ Sequence 4, Application US/09961400
/ Publication No. US20030124131A1
/ GENERAL INFORMATION:
/ APPLICANT: RYBAK, SUSANNA M.
/ APPLICANT: GOLDBERG, DAVID M.
/ APPLICANT: NEWTON, DIANNE L.
/ TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
/ FILE REFERENCE: 018733/1059
/ CURRENT APPLICATION NUMBER: US/09/961,400
/ CURRENT FILING DATE: 2001-09-25
/ PRIOR APPLICATION NUMBER: 09/622,613
/ PRIOR FILING DATE: 2000-08-17
/ PRIOR APPLICATION NUMBER: PCT/US99/06641
/ PRIOR FILING DATE: 1999-03-26
/ PRIOR APPLICATION NUMBER: 60/079,751
/ PRIOR FILING DATE: 1998-03-26
/ NUMBER OF SEQ ID NOS: 43
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 4
/ LENGTH: 104
/ TYPE: PRT
/ ORGANISM: Rana pipiens
US-09-961-400-4
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```
Query Match          96.9%; Score 562; DB 11; Length 104;
Best Local Similarity 98.1%; Pred. No. 7,1e-57;
Matches 102; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 QDMLTFQKHLLNTRDVDCNNILSTNLFPHCKDKNTFIYSRPEPVKAICKGIISKVLT 61
Db 1 QDMLTFQKHLLNTRDVDCNNILSTNLFPHCKDKNTFIYSRPEPVKAICKGIISKVLT 60

Qy 62 SEFYISDCNVTSRPCKYKLLKKSSTTFCTVCENQAPVHFVGHC 105
Db 61 FEFYISDCNVTSRPCKYKLLKKSSTTFCTVCENQAPVHFVGHC 104
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RESULT 14
US-09-948-391A-11
/ Sequence 11, Application US/09948391A
/ Publication No. US20030027311A1
/ GENERAL INFORMATION:
/ APPLICANT: Rybak, Susanna M.
/ APPLICANT: Newton, Dianne L.
/ APPLICANT: The United States of America
/ APPLICANT: as represented by The Secretary of the
/ APPLICANT: Department of Health and Human Services
/ TITLE OF INVENTION: Recombinant Anti-Tumor RNase
/ FILE REFERENCE: 015280-343110US
/ CURRENT APPLICATION NUMBER: US/09/948,391A
/ CURRENT FILING DATE: 2002-05-10
/ PRIOR APPLICATION NUMBER: US 60/079,751
/ PRIOR FILING DATE: 1998-03-27
/ PRIOR APPLICATION NUMBER: WO PCT/US99/06641
/ PRIOR FILING DATE: 1999-03-26
/ PRIOR APPLICATION NUMBER: US 09/622,613
/ PRIOR FILING DATE: 2000-08-17
/ NUMBER OF SEQ ID NOS: 43
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 11
/ LENGTH: 104
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:Rana pipiens
/ OTHER INFORMATION: ribonuclease with Gln1ser substitution
/ OTHER INFORMATION: (recombinant RapLRI Q1S)
US-09-948-391A-11
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Query Match          96.7%; Score 561; DB 11; Length 104;
Best Local Similarity 98.1%; Pred. No. 9,3e-57;
Matches 101; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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Qy 3 DMLTFQKHLLNTRDVDCNNILSTNLFPHCKDKNTFIYSRPEPVKAICKGIISKVLT 62
Db 2 DMLTFQKHLLNTRDVDCNNILSTNLFPHCKDKNTFIYSRPEPVKAICKGIISKVLT 61

Qy 63 EFYISDCNVTSRPCKYKLLKKSSTTFCTVCENQAPVHFVGHC 105
Db 62 EFYISDCNVTSRPCKYKLLKKSSTTFCTVCENQAPVHFVGHC 104
```

```
RESULT 15
US-09-961-400-11
/ Sequence 11, Application US/09961400
/ Publication No. US20030124131A1
/ GENERAL INFORMATION:
/ APPLICANT: RYBAK, SUSANNA M.
/ APPLICANT: GOLDBERG, DAVID M.
/ APPLICANT: NEWTON, DIANNE L.
/ TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
/ FILE REFERENCE: 018733/1059
/ CURRENT APPLICATION NUMBER: US/09/961,400
/ CURRENT FILING DATE: 2001-09-25
/ PRIOR APPLICATION NUMBER: 09/622,613
/ PRIOR FILING DATE: 2000-08-17
/ PRIOR APPLICATION NUMBER: PCT/US99/06641
/ PRIOR FILING DATE: 1999-03-26
/ PRIOR APPLICATION NUMBER: 60/079,751
/ PRIOR FILING DATE: 1998-03-26
/ NUMBER OF SEQ ID NOS: 43
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 11
/ LENGTH: 104
/ TYPE: PRT
/ ORGANISM: Rana pipiens
US-09-961-400-11
```

Query Match 96.7%; Score 561; DB 11; Length 104;
 Best Local Similarity 98.1%; Pred. No. 9.3e-57;
 Matches 101; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy	3	DMLTFQKKHLNTRDVCNNILSTNLFHCKDKNTFIYSRPEPVKAI	CKGIIASKNVLTTS	62
Db	2	DMLTFQKKHLNTRDVCNNIMSTNLFHCKDKNTFIYSRPEPVKAI	CKGIIASKNVLTTS	61
Qy	63	EFYLSDCNVTSRPCKYKLLKSTIITFCVTCENQAPVHFGVGHC		105
Db	62	EFYLSDCNVTSRPCKYKLLKSTIITFCVTCENQAPVHFGVGHC		104

Search completed: January 22, 2004, 12:12:25
 Job time : 24.9719 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 22, 2004, 12:01:20 (Search time 11.7978 Seconds
(without alignments)
855.901 Million cell updates/sec

Title: US-09-622-613C-8
Perfect score: 580
Sequence: 1 MODMLTFQKXHLTNRDVC.....TFCVTCENQAPVHFGVGHG 105

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: PIR_76:.*
2: PIR1:.*
3: PIR2:.*
4: PIR3:.*
5: PIR4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	541	93.3	104 2 A39035	ribonuclease-relat
2	277	47.8	111 2 A27121	ribonuclease-relat
3	273.5	47.2	111 1 JX0120	ribonuclease-relat
4	257.5	44.4	111 2 JX0085	pancreatic ribonuc
5	143	24.7	119 2 S41111	pancreatic ribonuc
6	125	21.6	124 1 NRUI	pancreatic ribonuc
7	122	21.0	125 1 A32474	angiotensin valida
8	120	20.7	128 1 NRCU	pancreatic ribonuc
9	119	20.5	124 1 NRCU	pancreatic ribonuc
10	115.5	19.9	145 1 A35332	pancreatic ribonuc
11	114	19.7	128 1 NRKS	angiotensin precurs
12	113	19.5	125 1 B43825	angiotensin precurs
13	113	19.5	128 1 NRGPB	angiotensin - rabbi
14	111	19.1	124 1 NRCB	pancreatic ribonuc
15	110	19.0	124 1 NRYV	pancreatic ribonuc
16	109	18.8	147 1 NRHAG	angiotensin precurs
17	108	18.6	124 1 NRHP	pancreatic ribonuc
18	106.5	18.4	123 1 A43825	angiotensin - pig
19	106	18.3	124 1 NRBOB	pancreatic ribonuc
20	106	18.3	124 1 NRPG	pancreatic ribonuc
21	106	18.3	150 1 NRBO	pancreatic ribonuc
22	105.5	18.2	147 2 I52489	pancreatic ribonuc
23	105	18.1	124 2 S08549	ribonuclease 4 (EC
24	105	18.1	128 1 NRHO	ribonuclease 4 (EC
25	105	18.1	128 1 NRHO	pancreatic ribonuc
26	105	18.1	167 2 S20066	pancreatic ribonuc
27	104.5	18.0	155 2 JG6159	pancreatic ribonuc
28	103	17.8	124 1 NRSH	pancreatic ribonuc
29	103	17.8	124 1 NRPRH	pancreatic ribonuc

30	103	17.8	124 1 NRCPA	pancreatic ribonuc
31	103	17.8	124 2 S07141	pancreatic ribonuc
32	102	17.6	124 1 NRMB	pancreatic ribonuc
33	102	17.6	124 1 NRGN	pancreatic ribonuc
34	102	17.6	124 1 NRGM	pancreatic ribonuc
35	101	17.4	124 1 NRGP	pancreatic ribonuc
36	101	17.4	156 2 JG6160	eosinophil-associat
37	99	17.1	124 1 NRDEO	pancreatic ribonuc
38	99	17.1	124 1 NREKN	pancreatic ribonuc
39	99	17.1	124 1 NRCHM	pancreatic ribonuc
40	99	17.1	124 1 NRCHM	pancreatic ribonuc
41	99	17.1	128 1 NRCHM	pancreatic ribonuc
42	98	16.9	124 1 NRHY	pancreatic ribonuc
43	97	16.7	124 1 NRDR	pancreatic ribonuc
44	97	16.7	124 1 NRDN	pancreatic ribonuc
45	96	16.6	124 1 NRDEF	pancreatic ribonuc

ALIGNMENTS

RESULT 1

A39035 ribonuclease-related anti-tumor protein - northern leopard frog (fragment)
C/Species: Rana pipiens (northern leopard frog)
C/Date: 31-Jul-1991 #sequence_revision 31-Jul-1991 #text_change 30-Jun-1993
R/Accession: A39035
R/Ardelet, W.; Mikuleki, S.M.; Shogen, K.
J. Biol. Chem. 266, 245-251, 1991
A/Title: Amino acid sequence of an anti-tumor protein from Rana pipiens oocytes and earl
A/Reference number: A39035; MUID:91093131; PMID:1985896
A/Accession: A39035
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-104 <ARD>
C/Superfamily: pancreatic ribonuclease

Query Match 93.3% Score 541; DB 2; Length 104;
Best Local Similarity 93.3%; Pred. No. 2.4e-48;
Matches 97; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 2 QDWLTFQKXHLTNRDVCNNILSTNLFFCKDKNTFIYSRPEPVKAIKGIISKNVLT 61
DB 1 EDWLTFOKXHLTNRDVCDDNINSTNLFFCKDKNTFIYSRPEPVKAIKGIISKNVLT 60
QY 62 SEFYLSDCNVTSPCKYKXKSTITTCVTCENQAPVHFGVGHG 105
DB 61 SEFYLSDCNVTSPCKYKXKSTITTCVTCENQAPVHFGVGHG 104

RESULT 2

A27121 ribonuclease-related sialic acid-binding lectin - bullfrog
C/Species: Rana catesbeiana (bullfrog)
C/Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 30-Jun-1993
R/Accession: A27121
R/Titani, K.; Takio, K.; Kuwada, M.; Nitta, K.; Sakakibara, F.; Kanauchi, H.; Takayanagi
Biochemistry 26, 2189-2194, 1987
A/Title: Amino acid sequence of sialic acid-binding lectin from frog (Rana catesbeiana)
A/Reference number: A27121; MUID:87299649; PMID:3304421
A/Molecule type: protein
A/Accession: A27121
A/Residues: 1-111 <TIT>
C/Superfamily: pancreatic ribonuclease
C/Keywords: lectin

Query Match 47.8% Score 277; DB 2; Length 111;
Best Local Similarity 46.8%; Pred. No. 2.7e-21;
Matches 52; Conservative 18; Mismatches 33; Indels 8; Gaps 3;

QY 2 QDWLTFQKXHLTNRDVCNNILSTNLFFCKDKNTFIYSRPEPVKAIKGIISKNV 57
DB 1 ENMATFOQXHLTNRDVCNNILSTNLFFCKDKNTFIYSRPEPVKAIKGIISKNV 59

R:Bond, M.D.; Strydom, D.J.
 Biochemistry 28, 6110-6113, 1989
 A>Title: Amino acid sequence of bovine angiogenin.
 A:Reference number: A32474; PMID:89375344; PMID:2775757
 A:Accession: A32474
 A:Molecule type: protein
 A:Residues: 1-125 <BON>
 A:Experimental source: plasma
 R:Maes, P.; Damart, D.; Rommens, C.; Montreuil, J.; Spik, G.; Tartar, A.
 FEBS Lett 241, 41-45, 1988
 A>Title: The complete amino acid sequence of bovine milk angiogenin.
 A:Reference number: S02001; PMID:89065101; PMID:3197838
 A:Accession: S02001
 A:Molecule type: protein
 A:Residues: 1-125 <MAE>
 A:Experimental source: milk
 R:Acharya, K.R.; Shapiro, R.; Riordan, J.F.; Vallee, B.L.
 submitted to the Brookhaven Protein Data Bank, January 1995
 A:Reference number: A65065; PDB:1ACI
 A:Contents: annotation; X-ray crystallography, 1.5 angstroms, residues 1-125
 R:Acharya, K.R.; Shapiro, R.; Riordan, J.F.; Vallee, B.L.
 Proc. Natl. Acad. Sci. U.S.A. 92, 2949-2953, 1995
 A>Title: Crystal structure of bovine angiogenin at 1.5 Angstrom resolution.
 A:Reference number: A58315; PMID:9524057; PMID:7708754
 A:Contents: annotation; X-ray crystallography, 1.5 angstroms
 R:Legin, O.; Albaret, C.; Bonems, F.; Spik, G.; Lallemand, J.Y.
 submitted to the Brookhaven Protein Data Bank, April 1996
 A:Reference number: A65709; PDB:1G1O
 A:Contents: annotation; conformation by (1)H-NMR, residues 1-125
 R:Legin, O.; Albaret, C.; Bonems, F.; Spik, G.; Lallemand, J.Y.
 Biochemistry 35, 8870-8880, 1996
 A>Title: Solution structure of bovine angiogenin by (1)H nuclear magnetic resonance spectroscopy.
 A:Reference number: A58821; PMID:96280645; PMID:8688423
 A:Contents: annotation; conformation by (1)H-NMR
 R:Reisdorf, C.; Abergl, D.; Bonems, F.; Lallemand, J.Y.; Decottignies, J.P.; Spik, G.
 Eur. J. Biochem. 224, 811-822, 1994
 A>Title: Proton resonance assignments and secondary structure of bovine angiogenin.
 A:Reference number: S48212; PMID:95010071; PMID:7925406
 A:Contents: annotation; conformation by (1)H-NMR
 C:Function:
 A:Description: hydrolyzes tRNA; induces vascularization of normal and malignant tissues
 C:Superfamily: pancreatic ribonuclease
 C:Keywords: angiogenesis; hydrolase; nucleic acid degradation
 F:60-68/Region: receptor binding #status predicted
 F:14,41,115/Active site: His, Tyr, His #status predicted
 F:127-82,40-93,58-108/Disulfide bonds: #status experimental

	Query Match	21.0%; Score 122; DB 1;	Length 125;
	Best Local Similarity	33.0%; Pred. No. 2.2e-05;	
	Matches	32; Conservative 15; Mismatches 32; Indels 18; Gaps 5;	
OY	17 DVDGNILSTLFL--HCKDKNTFYISRPPEVKAICKGIATSKN-----VLTTSEFYL 66	:: :	:: :
b	24 DEYFNMMKMKRLRTPRCQDRMTFIHGNDKDIAICE----DRNGPYRGDIRISKSEFOI 79	:: :	:: :
OY	67 SDG---NVTSR-PCKYKLKKSTIFCVTCENGAQAVHF 99	: :: :	:: :
D	80 TICCHKGGSSRPFRCYGATEDSRIVVGCEGLPVHF 116	: :: :	:: :

RESULT 8
 NRCU
 Pancreatic ribonuclease (EC 3.1.27.5) - nutria (tentative sequence)
 N:Alternate names: RNase 1; RNase A
 C:Species: Myocastor coypus (nutria, coypu)
 C>Date: 24-Apr-1994 #sequence_revision 30-Sep-1988 #text_change 31-Mar-2000
 A:Accession: A00822
 R:van den Berg, A.; van den Hende-Timmer, L.; Beintema, J.J.
 Biochim. Biophys. Acta 453, 400-409, 1976
 A>Title: Isolation, properties and primary structure of coypu and chinchilla pancreatic
 A:Reference number: A90612; MUID:77065676; PMID:999896
 A:Accession: A00822
 A:Molecule type: protein

A:Residues: 1-128 <VAN>
C:Superfamily: pancreatic ribonuclease
K:Keywords: glycoprotein; hydrolyase; nucleic acid digestion; pancreas
F.12.41.119.Active site: His_lys His #status predicted
P.26-84,40-95,58-110,65-72/Dissulfide bonds: #status predicted
F.734/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 20.7%; Score 120; DB 1; Length 128;
Best Local Similarity 29.1%; Pred. No. 3,5e+05;
Matches 34; Conservative 19; Mismatches 36; Indels 28; Gaps 7.

OY 7 FOKGHL-----TNRDVCNNIL-STLNF--HCKDKNFIYSRPEPKAICIGITASKV 58
|:::| |:::| |:::| |:::| |:::| |:::|
DB 8 FERGHMSRGSPSTNPNCVENMKSMRNMTQGRCKRPVNTFHVEPLADVGAVC----FGKNV 63
|:::| |:::| |:::| |:::| |:::| |:::|
OY 59 L-----TTSEFYISDCDNYSRP---CYKKLKSTTFICYTCENO--APHF 99
|:::| |:::| |:::| |:::| |:::| |:::|
DB 64 LCKKGQTNCTCVSNSSNMHTIDCRATVSNSDYPCNGCSRTISOEEKSIIVACGNPFVPVFH 120
|:::| |:::| |:::| |:::| |:::| |:::|

```

RESULT 9
NRMHK
pancreatic ribonuclease (EC 3.1.27.5) - minke whale
N:Alternate names: RNase 1; RNase A
C:Species: Balaenoptera acutorostrata (minke whale, lesser rorqual)
C:Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 03-Jun-1994
A:Accession: A00818
R:Emmens, M.; Welling, G.W.; Beintema, J.J.
Biochem. J. 157, 317-323, 1976
A:Title: The amino acid sequence of pike whale (lesser rorqual) pancreatic ribonuclease
A:Reference number: A00818; MUID:76277855; PMID:962870
A:Accession: A00818
A:Molecule type: protein
A:Residues: 1-124 <EMM>
C:Superfamily: pancreatic ribonuclease
C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F:12,41,119/Active site: His, Lys, His #status predicted
F:26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted
F:76/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental

Query Match 20.5%; Score 119; DB 1; Length 124;
Best Local Similarity 27.7%; Pred. No. 4.3e-05;
Matches 33; Conservative 16; Mismatches 42; Indels 28; Gaps 6;

OY 5 LTFQKHLLTNRDVD-----CNNILSTNLF---HCKDKNFTFVSRPEPVKAIKGIASK 56
    |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 6 MKFQKHMDSGNSPGNNPNYCNQMMRRKKYTCGRCKEVTNFVHSLSDVKAVC-----SOK 61
    |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

OY 57 NVL-----TTSEFLSDCNVTSRP---CKYLKASTITFCVTCENQ--APVHF 99
    |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 62 NVLCKGRTRNCVESNSTHMITDCRQTGGSSKYPICAVKTSQKEKHIIYACDEGNPNYPVHF 120
    |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 10
A35932
angiogenin precursor - mouse
N:Alternate names: angiogenesis factor
N:Contains: ribonuclease (EC 3.1.27.-)
C:Species: Mus musculus (house mouse)
C:Date: 09-Nov-1990 #sequence_revision 09-Nov-1990 #text_change 18-Jun-1999
A:Accession: A35932
R:Bond, M.D.; Vallee, B.L.
Biochem. Biophys. Res. Commun. 171, 988-995, 1990
A:Title: Isolation and sequencing of mouse angiogenin DNA.
A:Reference number: A35932; MUID:91025023; PMID:2222458
A:Accession: A35932
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-145 <BON>
A:Cross-references: GB:U22516; NID:g726325; PIDN:AAA91366.1; PID:g726326
C:Genetics:
A:Introns: #status absent
A:Function:

```

C:Superfamily: pancreatic ribonuclease
C:Keywords: pyroglutamic acid
F.1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Best local Similarity 26.1%; Pred. No. 0.00029;
Matches 31; Conservative 20; Mismatches 40; Indels 28; Gaps 6;

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OM protein - protein search, using sw model

Run on: January 22, 2004, 12:01:20 ; Search time 6.29213 Seconds
(without alignments)
784.758 Million cell updates/sec

Title: US-09-622-613C-8
Perfect score: 580
Sequence: 1 MODWLTFQKH/LTNRDVC.....TFCVTCENQAPVHFGVGHG 105

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	544	93.8	104	1	RN30_RANPI
2	280	48.3	111	1	RNPO_RANCA
3	273.5	47.2	111	1	LECS_RANCA
4	257.5	44.4	111	1	RNPL_RANCA
5	143	24.7	119	1	RNP_IGUG
6	127.5	22.0	145	1	ANGR_MOUSE
7	127.5	22.0	145	1	ANGI_MOUSE
8	125	21.6	124	1	RNP_GALMU
9	122	21.0	148	1	ANGI_BOVIN
10	120	20.7	128	1	RNP_MYOCO
11	119	20.5	124	1	RNP_BALAC
12	118.5	20.4	146	1	ANGI_MACMG
13	115.5	19.9	145	1	ANGI_MOUSE
14	115.5	19.9	146	1	ANGI_PAPHA
15	114	19.7	128	1	RNP_PROGU
16	113	19.5	125	1	ANGI_RABIT
17	113	19.5	128	1	RNPB_CAVPO
18	111	19.1	124	1	RNP_CHIBR
19	110	19.0	128	1	RNP_HYDHY
20	110	19.0	146	1	ANGI_MIOTA
21	110	19.0	156	1	ECR3_MOUSE
22	109	18.8	147	1	ANGI_HUMAN
23	109	18.8	147	1	ANGI_PANTR
24	108	18.6	124	1	RNP_HIPAM
25	106.5	18.4	123	1	ANGI_PIG
26	106	18.3	124	1	RNP_PIG
27	106	18.3	150	1	RNP_BOVIN
28	106	18.3	156	1	RNP_MYOG
29	105.5	18.2	147	1	RNS4_HUMAN
30	105	18.1	128	1	RNP_HYSCR
31	105	18.1	128	1	RNP_HYSCR
32	105	18.1	146	1	ANGI_SAGOE
33	105	18.1	167	1	RNBR_BOVIN

34	104.5	18.0	150	1	RNS6_SAIISC	O46529 saimiri sci
35	104.5	18.0	155	1	ECPI_MOUSE	P97426 mus musculu
36	104	17.9	141	1	RNBR_GIRCA	O29542 giraffa cam
37	104	17.9	146	1	ANGI_SAIISC	O8w60 saimiri sci
38	104	17.9	151	1	RNBR_AXIPR	PR7350 axis porcin
39	103	17.8	123	1	ANG2_BOVIN	P080929 bos taurus
40	103	17.8	124	1	RNPA_CAVPO	P06678 cavia porce
41	103	17.8	124	1	RNP_AEPME	P07847 aepyceros m
42	103	17.8	124	1	RNP_ANTAM	P06668 antilocapra
43	103	17.8	124	1	RNP_SHEEP	P00651 ovis aries
44	102	17.6	124	1	RNP_BUBBU	P00657 bubalus bub
45	102	17.6	124	1	RNP_CAMDR	P00670 camelus dro

ALIGNMENTS

RESULT 1	ID	RN30_RANPI	STANDARD;	PRT;	104 AA.
AC	P22069;				
DT	01-AUG-1991 (Rel. 19, Created)				
DT	01-FEB-1994 (Rel. 28, Last sequence update)				
DT	28-FEB-2003 (Rel. 41, Last annotation update)				
DE	P-30 protein (EC 3.1.27.-) (Onconase).				
OS	Rana pipiens (Northern leopard frog).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana;				
OX	NCBI_TaxID=8404;				
RN	[1]				
RP	SEQUENCE.				
RC	TISSUE=Embryo;				
RX	MEDLINE=9109311; PubMed=1985896;				
RA	Ardelet W., Mikulski S.M., Shogen K.;				
RT	"Amino acid sequence of an anti-tumor protein from Rana pipiens oocytes and early embryos. Homology to pancreatic ribonucleases.";				
RL	J. Biol. Chem. 266:245-251(1991).				
RN	[2]				
RP	3D-STRUCTURE MODELING.				
RX	MEDLINE=93066156; PubMed=1438177;				
RA	Mosmann S.C., Johns K.L., Ardelet W., Mikulski S.M., Shogen K.,				
RA	James M.N.G.;				
RT	"Comparative molecular modeling and crystallization of P-30 protein: a novel antitumor protein of Rana pipiens oocytes and early embryos.";				
RL	Proteins 14:392-400(1992).				
RN	[3]				
RP	X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).				
RX	MEDLINE=94166079; PubMed=8120892;				
RA	Mosmann S.C., Ardelet W., James M.N.G.;				
RT	"Refined 1.7 A X-ray crystallographic structure of P-30 protein, an amphibian ribonuclease with anti-tumor activity.";				
RL	J. Mol. Biol. 236:1141-1153(1994).				
CC	-1- FUNCTION: BASIC PROTEIN WITH ANTIPROLIFERATIVE/CYTOTOXIC ACTIVITY AGAINST SEVERAL TUMOR CELL LINES IN VITRO, AS WELL AS ANTITUMOR IN VIVO. IT EXHIBITS A RIBONUCLEASE-LIKE ACTIVITY AGAINST HIGH MOLECULAR WEIGHT RIBOSOMAL RNA.				
CC	-1- DEVELOPMENTAL STAGE: EARLY EMBRYOS (UP TO FOUR BLASTOMERE STAGE).				
CC	-1- SIMILARITY: Belongs to the pancreatic ribonuclease family.				
DR	PDB; 1ONC; 31-JAN-94.				
DR	InterPro; IPR001427; RNaseA.				
DR	Pfam; PF00074; RNaseA; 1.				
DR	ProDom; PD000535; RNaseA; 1.				
DR	SMART; SMO0092; RNaseA; 1.				
DR	PROSITE; PS00127; RNASE_PANCREATIC; 1.				
KW	Hydrolase; Nuclease; Endonuclease; 3D-structure;				
KW	Pyroliidone carboxylic acid.				
FT	MOD RES	1	10		PYRROLIDONE CARBOXYLIC ACID.
FT	ACT SITE	31	31		
FT	ACT SITE	97	97		
FT	ACT SITE	19	68		
FT	DISULFID	30	75		

FT DISULFID 48 90
 FT DISULFID 87 104
 FT HELIX 3 10
 FT STRAND 11 12
 FT HELIX 19 22
 FT TURN 23 24
 FT TURN 26 30
 FT STRAND 33 38
 FT HELIX 41 45
 FT HELIX 46 48
 FT TURN 49 50
 FT STRAND 55 58
 FT STRAND 63 70
 FT TURN 74 75
 FT STRAND 77 84
 FT STRAND 86 91
 FT TURN 92 93
 FT STRAND 94 101
 SQ SEQUENCE 104 AA; 11845 MW; 22A753C2F9E566B4 CRC64;

Query Match 93.8%; Score 544; DB 1; Length 104;
 Best Local Similarity 94.2%; Pred. No. 1.3e-52;
 Matches 98; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 QDWLTQKHLTNRDVDCNNILSTNLFHCKDKNTFIYSRPEPYKAIKGIISKVLT 61
 DB 1 QDWLTQKHLTNRDVDCNNILSTNLFHCKDKNTFIYSRPEPYKAIKGIISKVLT 60
 QY 62 SEFYLSDCNVTSRPCKYKLLKKSITTFCTGCENQAPVHFGVGHG 105
 DB 61 SEFYLSDCNVTSRPCKYKLLKKSITTFCTGCENQAPVHFGVGHG 104

RESULT 2

ID RNPO RANCA STANDARD; PRT; 111 AA.
 AC P11916;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ribonuclease, oocytes (EC 3.1.27.-) (RC-Knase) (sialic acid-binding lectin) (SBL-C).
 OS Rana catesbeiana (Bull frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
 OX NCBI_TaxID=8400;
 RN (1)
 RP SEQUENCE.
 RC TISSUE=Egg;
 RX MEDLINE=8729649; PubMed=3304421;
 RA Titani K., Takio K., Kuwada M., Nitte K., Sakakibara F., Kawachi H., Takayanagi G., Hakomori S.,
 RT "Amino acid sequence of sialic acid binding lectin from frog (Rana catesbeiana) eggs.";
 RL Biochemistry 26:2189-2194(1987).
 RN (2)
 RP CHARACTERIZATION, AND SEQUENCE OF 59-79.
 RX MEDLINE=92220613; PubMed=1373237;
 RA Liao Y.-D.;
 RT "A pyrimidine-guanine sequence-specific ribonuclease from Rana catesbeiana (bullfrog) oocytes.";
 RL Nucleic Acids Res. 20:1371-1377(1992).
 RN (3)
 RP CHARACTERIZATION.
 RC TISSUE=Egg;
 RX MEDLINE=93192604; PubMed=8448385;
 RA Nitte K., Oyama F., Oyama R., Sekiguchi K., Kawachi H., Takayanagi Y., Hakomori S., Titani K.;
 RT "Ribonuclease activity of sialic acid-binding lectin from Rana catesbeiana eggs.";
 RL Glycobiology 3:37-45(1993).
 RN (4)
 RP STRUCTURE BY NMR.

RX MEDLINE=98437383; PubMed=9761686;
 RA Chang C.-F., Chen C., Chen Y.-C., Hom K., Huang R.-F., Huang T.H.;
 RT "The solution structure of a cytotoxic ribonuclease from the oocytes of Rana catesbeiana (bullfrog).";
 RL J. Mol. Biol. 283:231-244(1998).
 CC -1- FUNCTION: Preferentially cleaves single-stranded RNA at pyrimidine as substrates, and prefers the former. The S-lectins in frog eggs may be involved in the fertilization and development of the frog embryo. This lectin agglutinates various animal cells, including normal lymphocytes, erythrocytes, and fibroblasts of animal and human origin.
 CC -1- SUBUNIT: Monomer.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the pancreatic ribonuclease family.
 DR PIR; A27121; A27121.
 DR PDB; 1BC4; 28-OCT-98.
 DR PDB; 1M07; 21-JAN-03.
 DR InterPro; IPR001427; RNASEA.
 DR Pfam; PF00074; rnaasea; 1.
 DR ProDom; PD000535; RNaseA; 1.
 DR SMART; SM00092; RNase_Pc; 1.
 DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
 KM Hydrolyase; Nuclease; Endonuclease; Sialic acid; lectin; 3D-structure; Pyroliadone carboxylic acid.
 FT MOD RES 1 1
 FT ACT SITE 10 10
 FT ACT SITE 35 35
 FT ACT SITE 103 103
 FT DISULFID 19 71
 FT DISULFID 34 81
 FT DISULFID 52 96
 FT DISULFID 93 110
 FT HELIX 3 10
 FT HELIX 19 23
 FT TURN 26 27
 FT STRAND 37 41
 FT STRAND 45 51
 FT HELIX 52 52
 FT TURN 57 62
 FT STRAND 68 73
 FT STRAND 83 88
 FT STRAND 92 97
 FT TURN 98 99
 FT STRAND 100 107
 SQ SEQUENCE 111 AA; 12464 MW; 0BC9E5F55729ECF4 CRC64;
 Query Match 48.3%; Score 280; DB 1; Length 111;
 Best Local Similarity 47.7%; Pred. No. 8.3e-24;
 Matches 53; Conservative 17; Mismatches 33; Indels 8; Gaps 3;
 QY 2 QDWLTQKHLTNRDVDCNNILSTNLF---HCKDKNTFIYSRPEPYKAIKGIISKV 57
 DB 1 QDWLTQKHLTNRDVDCNNILSTNLF---HCKDKNTFIYSRPEPYKAIKGIISKV 59
 QY 58 VLTSEFYLSDC---NVTSRPCKYKLLKKSITTFCTGCENQAPVHFGVGHG 105
 DB 60 VLTSEFYLSDC---NVTSRPCKYKLLKKSITTFCTGCENQAPVHFGVGHG 110
 RESULT 3
 LECG RANJA STANDARD; PRT; 111 AA.
 ID LECG RANJA
 AC P18839;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Sialic acid-binding lectin (EC 3.1.27.-).
 OS Rana japonica (Japanese reddish frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
 OX NCBI_TaxID=8402;
 RN (1)

SEQUENCE, AND DISULFIDE BONDS.

RC TISSUE=Egg;

RA MEDLINE=9103519; PubMed=2229005;

RA Kamiya Y., Oyama F., Sakakibara F., Nitta K., Kawachi H.,

RA Takayanagi Y., Titani K.;

RT "Amino acid sequence of a lectin from Japanese frog (Rana japonica) egg";

RL J. Biochem. 108:139-143(1990).

CC -1- FUNCTION: THE S-LECTINS IN FROG EGGS MAY BE INVOLVED IN THE FERTILIZATION AND DEVELOPMENT OF THE FROG EMBRYO. THIS LECTIN PREFERENTIALLY AGGLUTINATE A LARGE VARIETY OF TUMOR CELLS, BUT IT DOES NOT AGGLUTINATE NON-TRANSFORMED CELLS AND ERYTHROCYTES.

CC -1- SUBUNIT: Monomer.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- SIMILARITY: Belongs to the pancreatic ribonuclease family.

DR PIR: JX0120; JX0120.

DR HSSP: P11916; 1BC4.

DR InterPro: IPR001427; RNaseA.

DR Pfam: PF00074; rnaasea.1.

DR ProDom: PD000535; RNaseA.1.

DR SMART: SM00092; RNase_Pc.1.

DR PROSITE: PS00127; RNASE_PANCREATIC.1.

KM Hydrolyase; Nuclease; Endonuclease; Sialic acid; Lectin;

KM Pyrrolidone carboxylic acid.

FT MOD_RES 1 1

FT ACT_SITE 10 10 BY SIMILARITY.

FT ACT_SITE 35 35 BY SIMILARITY.

FT ACT_SITE 104 104 BY SIMILARITY.

FT DISULFID 19 72

FT DISULFID 34 82

FT DISULFID 52 97

FT DISULFID 94 111

SO SEQUENCE 111 AA; 12326 MW; FDEBDF3834ED679 CRC64;

Query Match 47.2%; Score 273.5; DB 1; Length 111;

Best Local Similarity 43.2%; Pred. No. 4.3e-23;

Matches 48; Conservative 20; Mismatches 36; Indels 7; Gaps 2;

OY 2 QDMLTFQKHLNTRDVCNMLSTNLF---HCKDKNTFYISRPPEVKAICKGIASKN 57

DB 1 QNMAFKEGHIINTNINCNTIMDKSIYVGGCKEKERNFTIISBDNVAKICSGASPNRN 60

OY 58 VITSEFYLSDC---NVTSRPCKYKLUKSTIFCYTCENQAVHFGVCHC 105

DB 61 VLSTRFQNLTCIRSATAPPCPYNSTRFTNVIQVCKENRLEPHVHFGIGRC 111

RESULT 4

RNPL_RANCA STANDARD; PRT; 111 AA.

AC P14626;

DT 01-APR-1990 (Rel. 14, Created)

DT 01-FEB-1994 (Rel. 28, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Ribonuclease, liver (EC 3.1.27.5).

OS Rana catesbeiana (Bull. frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.

OX NCBI_TaxID=8400;

RN NCBI_TaxID=8400;

RP SEQUENCE.

RC TISSUE=Liver;

RX MEDLINE=90130374; PubMed=2613682;

RX Nitta R., Katayama N., Okabe Y., Iwama M., Watanabe H., Abe Y.,

RA Okazaki T., Ohgi K., Irie M.;

RT "Primary structure of a ribonuclease from bullfrog (Rana catesbeiana) liver";

RL J. Biochem. 106:729-735(1989).

CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-phosphates and 3'-phosphooligonucleotides ending in C-P or U-P with 2',3'-cyclic phosphate intermediates.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- SIMILARITY: Belongs to the pancreatic ribonuclease family.

DR PIR: JX0085; JX0085.

DR HSSP: P11916; 1BC4.

DR InterPro: IPR001427; RNaseA.

DR Pfam: PF00074; rnaasea.1.

DR ProDom: PD000535; RNaseA.1.

DR SMART: SM00092; RNase_Pc.1.

DR PROSITE: PS00127; RNASE_PANCREATIC.1.

KM Hydrolyase; Nuclease; Endonuclease; Pyrrolidone carboxylic acid.

FT MOD_RES 1 1

FT ACT_SITE 10 10 BY SIMILARITY.

FT ACT_SITE 35 35 BY SIMILARITY.

FT ACT_SITE 104 104 BY SIMILARITY.

FT DISULFID 19 72

FT DISULFID 34 82

FT DISULFID 52 97

FT DISULFID 94 111

SO SEQUENCE 111 AA; 12461 MW; D64BA72456C10788 CRC64;

Query Match 44.4%; Score 257.5; DB 1; Length 111;

Best Local Similarity 41.4%; Pred. No. 2.4e-21;

Matches 46; Conservative 20; Mismatches 38; Indels 7; Gaps 2;

OY 2 QDMLTFQKHLNTRDVCNMLSTNLF---HCKDKNTFYISRPPEVKAICKGIASKN 57

DB 1 QNMAFKEGHIINTNINCNTIMDKSIYVGGCKEKERNFTIISBDNVAKICSGASPNRN 60

OY 58 VITSEFYLSDC---NVTSRPCKYKLUKSTIFCYTCENQAVHFGVCHC 105

DB 61 VLSTRFQNLTCIRSATAPPCPYNSTRFTNVIQVCKENRLEPHVHFGIGRC 111

RESULT 5

RNPL_IGUG STANDARD; PRT; 119 AA.

AC P80287;

DT 01-FEB-1994 (Rel. 28, Created)

DT 01-FEB-1994 (Rel. 28, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).

OS Iguana iguana (Common iguana).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Lepidodermata; Squamata; Iguania; Iguanidae; Iguaninae; Iguana.

OX NCBI_TaxID=8517;

RN NCBI_TaxID=8517;

RP SEQUENCE.

RC TISSUE=Pancreas;

RX MEDLINE=94139745; PubMed=8307028;

RX Zhao W., Beintema J.J., Hofsteenge J.;

RT "The amino acid sequence of iguana (Iguana iguana) pancreatic ribonuclease";

RT Eur. J. Biochem. 219:641-646(1994).

RL -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-phosphates and 3'-phosphooligonucleotides ending in C-P or U-P with 2',3'-cyclic phosphate intermediates.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- TISSUE SPECIFICITY: Pancreas.

CC -1- SIMILARITY: Belongs to the pancreatic ribonuclease family.

DR PIR: S41111; S41111.

DR HSSP: P00556; 1LSQ.

DR InterPro: IPR001427; RNaseA.

DR Pfam: PF00074; rnaasea.1.

DR PRINTS: PR00794; RIBONUCLEASE.

DR ProDom: PD000535; RNaseA.1.

DR SMART: SM00092; RNase_Pc.1.

DR PROSITE: PS00127; RNASE_PANCREATIC.1.

KM Hydrolyase; Nuclease; Endonuclease; Pyrrolidone carboxylic acid.

FT MOD_RES 1 1

FT ACT_SITE 10 10 BY SIMILARITY.

FT ACT_SITE 35 80 BY SIMILARITY.

FT DISULFID 39 91

FT DISULFID 57 106

FT ACT_SITE 10 10 BY SIMILARITY.

FT ACT_SITE 40 10 BY SIMILARITY.

FT ACT_SITE 113 113 BY SIMILARITY.

SO SEQUENCE 119 AA; 13324 MW; 6072PBB87B15BD5A CRC64;
 Query Match 24.7%; Score 143; DB 1; Length 119;
 Best Local Similarity 29.8%; Pred. No. 7.9e-09;
 Matches 34; Conservative 20; Mismatches 44; Indels 16; Gaps 5;
 QY 2 QDMLTQKHL-----TNRDVCNNIL---STNLFHCKDKTFTYSRPPVKAIC--K 50
 DB 1 QDWSSFKQKHIDYPTSSASNPAYCDLMQRRNLNPTKTRNTFVVASPSSEIQVCGSG 60
 QY 51 GIASKNVLTTSF-FYLSDC---NVTSPCKYKLLKSTTFCTCENQAPVHF 99
 DB 61 GTHYEDNLIDNSFIDLTCNKVNGTAPSSCKTNGPTKRIKRIACENNPVHF 114

RESULT 6

ANGR MOUSE STANDARD; PRT; 145 AA.
 AC 064438;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Angiogenin-related protein precursor.
 GN ANGRP.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129; TISSUE=Liver;
 RX MEDLINE=96079109; Pubmed=8530072;
 RA Brown W.E., Noble V., Subramanian V., Shapiro R.;
 RT "The mouse angiogenin gene family: structures of an angiogenin-related
 RT protein gene and two pseudogenes.";
 RL Genomics 29:200-206(1995).
 CC -1- SIMILARITY: Belongs to the pancreatic ribonuclease family.
 CC
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 CC
 CC EMBL: U2519; AAA91367.1; -
 CC DR HSSP: P03950; 1A4Y.
 CC DR MGD: MGI:104984; AngRP.
 CC DR InterPro: IPR001427; RNaseA.
 CC DR Pfam: PF00074; rnaaseA.1.
 CC DR PRINTS: PR00794; RIBONUCLEASE.
 CC DR ProDom: PD000535; RNaseA.1.
 CC DR SMART: SM00092; RNase_Pc.1.
 CC DR PROSITE: PS00127; RNASE_PANCREATIC.1.
 CC KM Signal: Hydrolase; Nuclease; Endonuclease;
 CC KM Pyroliadone carboxylic acid.
 CC FT SIGNAL 1 24 POTENTIAL.
 CC FT CHAIN 25 145 ANGIOENIN-RELATED PROTEIN.
 CC FT MOD_RES 25 25 PYROLIADONE CARBOXYLIC ACID (BY
 CC SIMILARITY).
 CC FT ACT_SITE 37 37 BY SIMILARITY.
 CC FT ACT_SITE 64 64 BY SIMILARITY.
 CC FT ACT_SITE 137 137 BY SIMILARITY.
 CC FT DISULFID 50 104 BY SIMILARITY.
 CC FT DISULFID 63 115 BY SIMILARITY.
 CC FT DISULFID 81 130 BY SIMILARITY.
 CC SO SEQUENCE 145 AA; 16612 MW; 29A6EB814429CAD CRC64;

Query Match 22.0%; Score 127.5; DB 1; Length 145;
 Best Local Similarity 38.2%; Pred. No. 4.8e-07;
 Matches 29; Conservative 11; Mismatches 29; Indels 7; Gaps 3;

QY 31 CDKXNFTYSRPPVKAIC--KGIASKNV-LTTSFYLSDCNVTSR-----PCKYKLLKS 83
 DB 63 CDVNTFHDITKXNKAICGKSGPYGRNLRIKSRFOVTTCTHKSRPPPCRYASKG 122
 QY 84 TTFCTCENQAPVHF 99
 DB 123 FRIITIGCENGPVHF 138

RESULT 7

ANGI CERAE STANDARD; PRT; 146 AA.
 AC 08N66;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Angiogenin precursor (EC 3.1.27.-) (Ribonuclease 5) (RNase 5).
 GN ANG OR RNASE5.
 OS Cercopithecus aethiops (Green monkey) (Grivet).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Cercopithecus.
 OX NCBI_TaxID=9534;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21918422; Pubmed=11919285;
 RA Zhang J., Rosenberg H.F.;
 RT "Diversifying selection of the tumor-growth promoter angiogenin in
 RT primate evolution.";
 RL Mol. Biol. Evol. 19:438-445(2002).
 CC -1- FUNCTION: MAY FUNCTION AS A TRNA-SPECIFIC RIBONUCLEASE THAT BINDS
 CC TO ACTIN ON THE SURFACE OF ENDOTHELIAL CELLS. ONCE BOUND,
 CC ANGIOENIN IS ENDOCYTOSED AND TRANSLOCATED TO THE NUCLEUS, THEREBY
 CC PROMOTING THE ENDOTHELIAL INVASIVENESS NECESSARY FOR BLOOD VESSEL
 CC FORMATION. ANGIOENIN INDUCES VASCULARIZATION OF NORMAL AND
 CC MALIGNANT TISSUES. ABOLISHES PROTEIN SYNTHESIS BY SPECIFICALLY
 CC HYDROLYZING CELLULAR TRNAS (By similarity).
 CC
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC
 CC -1- SIMILARITY: Belongs to the pancreatic ribonuclease family.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL: AF441664; AAL61646.1; -
 CC DR InterPro: IPR001427; RNaseA.
 CC DR Pfam: PF00074; rnaaseA.1.
 CC DR ProDom: PD000535; RNaseA.1.
 CC DR SMART: SM00092; RNase_Pc.1.
 CC DR PROSITE: PS00127; RNASE_PANCREATIC.1.
 CC KM Hydrolase; Nuclease; Endonuclease; Angiogenesis;
 CC KM Protein synthesis inhibitor; Signal; Pyroliadone carboxylic acid.
 CC FT SIGNAL 1 24 ANGIOENIN.
 CC FT CHAIN 25 146 PYROLIADONE CARBOXYLIC ACID (BY
 CC SIMILARITY).
 CC FT MOD_RES 25 25
 CC FT ACT_SITE 37 37 BY SIMILARITY.
 CC FT ACT_SITE 64 64 BY SIMILARITY.
 CC FT ACT_SITE 138 138 BY SIMILARITY.
 CC FT DISULFID 50 105 BY SIMILARITY.
 CC FT DISULFID 63 116 BY SIMILARITY.
 CC FT DISULFID 81 131 BY SIMILARITY.
 CC SO SEQUENCE 146 AA; 16444 MW; 27860112B85BDDF9 CRC64;

Query Match 22.0%; Score 127.5; DB 1; Length 146;
 Best Local Similarity 30.7%; Pred. No. 4.9e-07;
 Matches 31; Conservative 17; Mismatches 30; Indels 23; Gaps 4;
 QY 6 TFOKHLTNRDVCNNILSTNLFHCKDKNFTYSRPPVKAIC---KGIASKNV-LTT 61

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Db      53 TWRRRLTSP-----CKDINTFIHGRHRIKALICDENGPNVGENIRISK 97
Qy      62 SEFYLSDCNVT-----RCKYKTKSTIFCTCENQAPVH 98
Db      98 SPFOVTTCNLRGSPRPPCOYRATRGSRNMIWVCENGELPVH 138

RESULT 8
RNP_GALMU
ID      RNP_GALMU      STANDARD:      PRT:      124 AA.
AC      P00680;
DT      21-JUL-1986 (Rel. 01, Created)
DT      21-JUL-1986 (Rel. 01, Last sequence update)
DT      28-FEB-2003 (Rel. 41, Last annotation update)
DE      Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).
GN      RNASE1 OR RN51.
OS      Galea musteloides (Cui's).
OC      Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Hystriognathi; Cavidae; Galea.
OX      NCBI_TaxId=10146;
RN      [1]
RP      SEQUENCE.
RX      MEDLINE=87036770; PubMed=6571219;
RA      Beutema J.J., Neuteboom B.;
RT      "Origin of the duplicated ribonuclease gene in guinea-pig: comparison
RT      of the amino acid sequences with those of two close relatives:
RT      capybara and cuis ribonuclease.";
RL      J. Mol. Evol. 19:145-152(1983).
CC      -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
CC      phosphates and 3'-phosphonucleotides ending in C-P or U-P
CC      with 2',3'-cyclic phosphate intermediates.
CC      -1- SUBCELLULAR LOCATION: Secreted.
CC      -1- TISSUE SPECIFICITY: Pancreas.
CC      -1- SIMILARITY: Belongs to the pancreatic ribonuclease family.
DR      HSSP; P00656; ISRN.
DR      InterPro: IPR001427; RNaseA.
DR      Pfam; PF00074; rnaaseA; 1.
DR      PRINTS; PR00794; RIBONUCLEASE.
DR      ProDom; PD000535; RNaseA; 1.
DR      SMART; SM00092; RNase_Pc; 1.
DR      PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW      Hydrolase; Nuclease; Endonuclease.
FT      DISULFID 26 84 BY SIMILARITY.
FT      DISULFID 40 95 BY SIMILARITY.
FT      DISULFID 58 110 BY SIMILARITY.
FT      DISULFID 65 72 BY SIMILARITY.
FT      ACT_SITE 12 12 BY SIMILARITY.
FT      ACT_SITE 41 41 BY SIMILARITY.
FT      ACT_SITE 119 119 BY SIMILARITY.
FT      VARIANT 1 1 MISSING (IN 1/3 OF THE MOLECULES).
SQ      SEQUENCE 124 AA; 13870 MW; 609C7E51A7BBA25 CRC64;

Query Match 21.6%; Score 125; DB 1; Length 124;
Best Local Similarity 29.8%; Pred. No. 7.6e-07;
Matches 36; Conservative 19; Mismatches 34; Indels 32; Gaps 7;

Qy      5 LTFQKGL-----TNTRDVDCNNIL--STNLFHCKDXNFITSRPEVYAIKGIIA 54
Db      6 MKFOQHNDSDOHPTINTN--YCNEMVRRSMTGRCCKRVNFTVHEPLAVAVC-----S 59
Qy      55 SKNV-----LTSEFYLSDCNVTSRP-----CKYKTKSTIFCTCEN--QAPVH 98
Db      60 QKNVCKKNGQNTVCYQSHSSMRITDCRTVSSKYPCMSYRMTQAQSIIVACGTPSVPH 119
Qy      99 F 99
Db      120 F 120

RESULT 9
ANGI_BOVIN

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ID      ANGI_BOVIN      STANDARD:      PRT:      148 AA.
AC      P10152; O9GKP9;
DT      01-MAR-1989 (Rel. 10, Created)
DT      28-FEB-2003 (Rel. 41, Last sequence update)
DT      28-FEB-2003 (Rel. 41, Last annotation update)
DE      Angiogenin-1 precursor (EC 3.1.27.-).
GN      ANGI OR ANG.
OS      Bos taurus (Bovine).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC      Bovidae; Bovinae; Bos.
OX      NCBI_TaxId=9913;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Liver;
RA      Chang S.-I.;
RT      "Cloning, sequencing, and expression of bovine angiogenin.";
RL      Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN      [2]
RP      SEQUENCE OF 24-148.
RC      TISSUE=Milk;
RX      MEDLINE=89065101; PubMed=3197838;
RA      Maes P., Damart D., Rommens C., Montreuil J., Spik G., Tartar A.;
RT      "The complete amino acid sequence of bovine milk angiogenin.";
RL      FEBS Lett. 241:41-45(1988).
RN      [3]
RP      SEQUENCE OF 24-148.
RC      TISSUE=Plasma;
RX      MEDLINE=89375344; PubMed=2775757;
RA      Bond M.D., Strydom D.J.;
RT      "Amino acid sequence of bovine angiogenin.";
RL      Biochemistry 28:6110-6113(1989).
RN      [4]
RP      CHARACTERIZATION, AND SEQUENCE OF 25-55.
RC      TISSUE=Plasma;
RX      MEDLINE=89118214; PubMed=3064806;
RA      Bond M.D., Vallee B.L.;
RT      "Isolation of bovine angiogenin using a placental ribonuclease
RT      inhibitor binding assay.";
RL      Biochemistry 27:6282-6287(1988).
RN      [5]
RP      X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS).
RX      MEDLINE=95224057; PubMed=7708754;
RA      Acharya K.R., Shapiro R., Riordan J.F., Vallee B.L.;
RT      "Crystal structure of bovine angiogenin at 1.5-A resolution.";
RL      Proc. Natl. Acad. Sci. U.S.A. 92:2949-2953(1995).
RN      [6]
RP      STRUCTURE BY NMR.
RX      MEDLINE=96280645; PubMed=8688423;
RA      Leguin O., Albaret C., Bontems F., Spik G., Lallemand J.-Y.;
RT      "Solution structure of bovine angiogenin by 1H nuclear magnetic
RT      resonance spectroscopy.";
RL      Biochemistry 35:8870-8880(1996).
RN      [7]
RP      FUNCTION: MAY FUNCTION AS A tRNA-SPECIFIC RIBONUCLEASE THAT BINDS
RP      TO ACTIN ON THE SURFACE OF ENDOTHELIAL CELLS; ONCE BOUND,
RP      ANGIOGENIN IS ENDOCYTOSED AND TRANSLOCATED TO THE NUCLEUS, THEREBY
RP      PROMOTING THE ENDOGENOUS AND TRANSLOCATED TO THE NUCLEUS, THEREBY
RP      FORMATION. ANGIOGENIN INDUCES VASCULARIZATION OF NORMAL AND
RP      MALIGNANT TISSUES. ABOLISHES PROTEIN SYNTHESIS BY SPECIFICALLY
RP      HYDROLYZING CELLULAR TSNAS. BINDS TIGHTLY TO PLACENTAL
RP      RIBONUCLEASE INHIBITOR AND HAS VERY LOW RIBONUCLEASE ACTIVITY.
RN      [8]
RP      SUBCELLULAR LOCATION: Secreted.
RC      -1- TISSUE SPECIFICITY: SERUM, AND MILK.
RN      [9]
RP      -1- SIMILARITY: Belongs to the pancreatic ribonuclease family.
RN      [10]
RP      This SWISS-PROT entry is copyright. It is produced through a collaboration
RP      between the Swiss Institute of Bioinformatics and the EMBL outstation -
RP      the European Bioinformatics Institute. There are no restrictions on its
RP      use by non-profit institutions as long as its content is in no way
RP      modified and this statement is not removed. Usage by and for commercial
RP      entities requires a license agreement (See http://www.ebi.ac.uk/announce/
RP      or send an email to license@ebi.ac.uk).

```


Db 6 MKFORHMDSGNSPGNNPNVNCNMMRRKMTQGRCKPVNTFVHESLEDVAVC-----SQK 61
 Oy 57 NWL-----TSEFLSDCNVTSR-----CKTKLKKSTTTCVTGNC--AAVHP 99
 Db 62 NWLCKNGRTNCEYNSTHMTTDCRGTGSSKYPNCAYKTSQKXHIIVACEGNPYVHVF 120

RESULT 12

ANGI_MOUSE
 ID ANGI_MOUSE STANDARD; PRT; 146 AA.
 AC Q8WNG3;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Angiogenin precursor (EC 3.1.27.-) (Ribonuclease 5) (Rnase 5).
 GN ANG OR RNASE5.
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecidae; Macaca.
 OX NCBI_TaxID=9544;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21918422; PubMed=11919285;
 RA Zhang J., Rosenberg H.F.;
 RT "Diversifying selection of the tumor-growth promoter angiogenin in primate evolution";
 RL Mol. Biol. Evol. 19:438-445(2002).
 CC -1- FUNCTION: MAY FUNCTION AS A TRNA-SPECIFIC RIBONUCLEASE THAT BINDS TO ACTIN ON THE SURFACE OF ENDOTHELIAL CELLS; ONCE BOUND, ANGIOGENIN IS ENDOCYTOSED AND TRANSLOCATED TO THE NUCLEUS, THEREBY PROMOTING THE ENDOTHELIAL INVASIVENESS NECESSARY FOR BLOOD VESSEL FORMATION. ANGIOGENIN INDUCES VASCULARIZATION OF NORMAL AND MALIGNANT TISSUES. ABOLISHES PROTEIN SYNTHESIS BY SPECIFICALLY HYDROLYZING CELLULAR TRNAS (By similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the pancreatic ribonuclease family.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 CC
 CC EMBL: AF41667; AAL61649.1; -.
 CC InterPro: IPR001427; RNaseA.
 CC Pfam: PF00074; RNaseA; 1.
 CC ProDom: PD000535; RNaseA; 1.
 CC SMART: SM00092; RNase_Pc; 1.
 CC PROSITE: PS00127; RNASE_PANCREATIC; 1.
 CC DR Hydrolyase; Nuclease; Endonuclease; Angiogenesis;
 CC KM Protein synthesis inhibitor; Signal; Pyrolydine carboxylic acid.
 CC FT SIGNAL 1 24
 CC FT CHAIN 25 146
 CC FT MOD_RES 25 25
 CC FT ACT_SITE 37 37
 CC FT ACT_SITE 64 64
 CC FT ACT_SITE 138 138
 CC FT DISULFID 50 105
 CC FT DISULFID 63 116
 CC FT DISULFID 81 131
 CC SEQUENCE 146 AA; 16301 MW; E39A89215DB2A2A4 CRC64;

Query Match 20.4%; Score 118.5; DB 1; Length 146;
 Best Local Similarity 28.7%; Pred. No. 4.7e-06;
 Matches 29; Conservative 17; Mismatches 32; Indels 23; Gaps 4;

Oy 6 TFOKHLNTRDVCNNLSTLPHCKDKNTFYSRPEVKIC---AGIISKV-LTT 61
 Db 53 TWRRHLTSP-----CKDINTFVHGNNRHHTAIAGDENGSYPGMLRIST 97

Oy 62 SEFLYSDCNVTS-----RCKTKLKKSTTTCVTGNCQAPRH 98
 Db 98 SPFOVTTCKLRGSGPRPPCOYRATRGSRNIIWGCENGLPVH 138

RESULT 13

ANGI_MOUSE
 ID ANGI_MOUSE STANDARD; PRT; 145 AA.
 AC P21570;
 DT 01-MAY-1991 (Rel. 18, Created)
 DT 01-MAY-1991 (Rel. 18, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Angiogenin precursor (EC 3.1.27.-) (Ribonuclease 5) (Rnase 5).
 GN ANG.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91025023; PubMed=2222458;
 RA Bond M.D., Vallee B.L.;
 RT "Isolation and sequencing of mouse angiogenin DNA";
 RL Biochem. Biophys. Res. Commun. 171:988-995(1990).
 RN [2]
 RP PARTIAL SEQUENCE.
 RC TISSUE=serum;
 RX MEDLINE=91192291; PubMed=8448182;
 RA Bond M.D., Strydom D.J., Vallee B.L.;
 RT "Characterization and sequencing of rabbit, pig and mouse angiogenins: discernment of functionally important residues and regions";
 RL Biochim. Biophys. Acta 1162:177-186(1993).
 CC -1- FUNCTION: MAY FUNCTION AS A TRNA-SPECIFIC RIBONUCLEASE THAT BINDS TO ACTIN ON THE SURFACE OF ENDOTHELIAL CELLS; ONCE BOUND, ANGIOGENIN IS ENDOCYTOSED AND TRANSLOCATED TO THE NUCLEUS, THEREBY PROMOTING THE ENDOTHELIAL INVASIVENESS NECESSARY FOR BLOOD VESSEL FORMATION. ANGIOGENIN INDUCES VASCULARIZATION OF NORMAL AND MALIGNANT TISSUES. ABOLISHES PROTEIN SYNTHESIS BY SPECIFICALLY HYDROLYZING CELLULAR TRNAS.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the pancreatic ribonuclease family.

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 CC
 CC EMBL: U22516; AAA91366.1; -.
 CC PIR: A35932; A35932.
 CC HSSP: P03950; 1AAY.
 CC MGD: MGI:88022; Ang.
 CC InterPro: IPR001427; RNaseA.
 CC Pfam: PF00074; RNaseA; 1.
 CC PRINTS: PR00794; RIBONUCLEASE.
 CC ProDom: PD000535; RNaseA; 1.
 CC SMART: SM00092; RNase_Pc; 1.
 CC PROSITE: PS00127; RNASE_PANCREATIC; 1.
 CC KM Hydrolyase; Nuclease; Endonuclease; Angiogenesis;
 CC KW Protein synthesis inhibitor; Signal; Pyrolydine carboxylic acid.
 CC FT SIGNAL 1 24
 CC FT CHAIN 25 145
 CC FT MOD_RES 25 25
 CC FT ACT_SITE 37 37
 CC FT ACT_SITE 64 64
 CC FT ACT_SITE 137 137
 CC FT DISULFID 50 104
 CC DISULFID 63 115

Query Match 20.4%; Score 118.5; DB 1; Length 146;
 Best Local Similarity 28.7%; Pred. No. 4.7e-06;
 Matches 29; Conservative 17; Mismatches 32; Indels 23; Gaps 4;

Oy 6 TFOKHLNTRDVCNNLSTLPHCKDKNTFYSRPEVKIC---AGIISKV-LTT 61
 Db 53 TWRRHLTSP-----CKDINTFVHGNNRHHTAIAGDENGSYPGMLRIST 97

FT	DISULFID	81	130		BY SIMILARITY.
SQ	SEQUENCE	145 AA;	16228 MM;	06944260BB764938 CXC64;	
	Query Match		19.9%; Score 115.5; DB 1; Length 145;		
	Best Local Similarity	35.5%;	Pred. No. 9.8e-06;		
	Matches	27; Conservative	11; Mismatches	31; Indels	7; Gaps
OY		31	CKDKNTFYLSRPEPKAIC-KGIASGV-LTTFSEFLSDPNVTS-----PPCRYKLKKS	83	
			: : : : : : :		
Dd		63	CKDWNTHFGKNXNKAICGANGSPRYENLKMRSKPFVYTCTKGTGGSPRPCCYRASAG	122	
OY		84	TITFCVTGCNQAPVFH	99	
		:			
Dd		123	FRRVIACENGLPVHF	138	
	RESULT 14				
ANGL_PAPHA	ID	STANDARD:	PRT:	146 AA.	
AC	Q8WNG4;				
DT	28-FEB-2003 (Rel. 41, Created)				
DT	28-FEB-2003 (Rel. 41, Last sequence update)				
DT	28-FEB-2003 (Rel. 41, Last annotation update)				
DE	Angiogenin precursor (EC 3.1.27.-) (Ribonuclease 5) (RNase 5).				
GN	ANG OR RNASES.				
OS	Papio hamadryas (Hamadryas baboon).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;				
OC	Cercopithecinae; Papio.				
OX	NCBI_TaxID=9557;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=21918422; PubMed=11919285;				
RA	Zhang J., Rosenberg H.F.;				
RT	"Diverting selection of the tumor-growth promoter angiogenin in				
RL	primate evolution.";				
	Mol. Biol. Evol. 19:438-445(2002).				
CC	-I- FUNCTION: MAY FUNCTION AS A TRNA-SPECIFIC RIBONUCLEASE THAT BINDS				
CC	TO ACTIN ON THE SURFACE OF ENDOTHELIAL CELLS; ONCE BOUND,				
CC	ANGIOENDIN IS ENDOCYTOSED AND TRANSLOCATED TO THE NUCLEUS, THEREBY				
CC	PROMOTING THE ENDOTHELIAL INVASIVENESS NECESSARY FOR BLOOD VESSEL				
CC	FORMATION. ANGIOENDIN INDUCES VASCULARIZATION OF NORMAL AND				
CC	MALIGNANT TISSUES. ABOLISHES PROTEIN SYNTHESIS BY SPECIFICALLY				
CC	HYDROLYZING CELLULAR TMNAS (By similarity).				
CC	-I- SUBCELLULAR LOCATION: Secreted.				
CC	-I- SIMILARITY: Belongs to the pancreatic ribonuclease family.				
CC	This SWISS-PROT entry is copyright.				
CC	between the Swiss Institute of Bioinformatics and the EMBL Outstation-				
CC	The European Bioinformatics Institute. There are no restrictions on its				
CC	use by non-profit institutions as long as its content is in no way				
CC	modified and this statement is not removed. Usage by and for commercial				
CC	entities requires a license agreement (see http://www.isdb-sib.ch/announce/				
CC	or send an email to licenses@isdb-sib.ch).				
DR	EMBL: AF441666; AAL61648.1; -				
DR	InterPro: IPR001427: RNaseH.				
DR	Pfam: PF00074: rnaase_h.1.				
DR	Pfdom: PFOO0535: RNaseA.1.				
DR	SMART: SMO0092: RNase_Pc.1.				
DR	PROSITE: PS00127: RNASE_PANCREATIC.1.				
KM	Hydrolase; Nuclease; Endonuclease; Angiogenesis;				
KW	Protein synthesis inhibitor; Signal; Pyroglutamate carboxylic acid.				
FT	SIGNAL	1	24		
FT	CHAIN	25	146		
FT	MOD_RES	25	25		
FT	ACT_SITE	37	37		
FT	ACT_SITE	64	64		
FT	ACT_SITE	138	138		
FT	DISULFID	50	105		
FT	DISULFID	63	116		
FT	DISULFID	81	131		

[illegible]

ID	RNP_PROGU	STANDARD:	PRT:	128 AA.
AC	P04059			
DT	01-NOV-1986	(Rel. 03, Created)		
DT	01-NOV-1986	(Rel. 03, Last sequence update)		
DT	28-FEB-2003	(Rel. 41, Last annotation update)		
DE	Ribonuclease pancreatic (EC 3.1.27.5) (RNaase 1) (RNaase A)			
GN	RNASE1 OR RN51			
OS	Proechinys guaire (Castiagua)			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Hystriocognathi; Echimyidae; Proechimys			
OX	NCBI_TaxID=10163;			
RN	(1)			
RP	SEQUENCE			
RC	TISSUE=Pancreas;			
RX	MEDLINE=83000399; PubMed=7115727;			
RA	Beintema J.J., Knol G., Martens B.;			
RT	"The primary structures of pancreatic ribonucleases from African			
RT	porcupine and castiagua, two hystriocomorph rodent species."			
RL	Biochim. Biophys. Acta 705:102-110(1982).			
CC	-1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-			
CC	phosphates and 3'-phosphooligonucleotides ending in C-P or U-P			
CC	with 2',3'-cyclic phosphate intermediates.			
CC	-1- SUBCELLULAR LOCATION: Secreted.			
CC	-1- TISSUE SPECIFICITY: Pancreas.			
CC	-1- SIMILARITY: Belongs to the pancreatic ribonuclease family.			
DR	PIR: A00821; NRKS.			
DR	HSSP: P00656; 1SRN.			
DR	InterPro: IPR001427; RNaseA.			
DR	Pfam: PF00074; rnaaseA. 1.			
DR	PRINTS: P000794; RIBONUCLEASE.			
DR	ProDom: P000535; RNaseA; 1.			
DR	SMART: SMO0092; RNase_Pc; 1.			
DR	PROSITE: PS00127; RNASE_PANCREATIC; 1.			
KW	Hydrolase; Nuclease; Endonuclease; Glycoprotein.			
FT	DISULFID 26	84	BY SIMILARITY.	
FT	DISULFID 40	95	BY SIMILARITY.	
FT	DISULFID 58	110	BY SIMILARITY.	
FT	DISULFID 65	72	BY SIMILARITY.	
FT	ACT_SITE 12	12	BY SIMILARITY.	
FT	ACT_SITE 41	41	BY SIMILARITY.	
FT	ACT_SITE 119	119	BY SIMILARITY.	
FT	CABOHD 34	34	N-LINKED (GLCNAC. . .).	
SQ	SEQUENCE 128 AA; 14244 MW; 2D858093A9D3C936 CRC64;			
Query Match	19.7%;	Score 114;	DB 1;	Length 128;
Best Local Similarity	29.1%;	Fred. NO. 1.2e-05;		
Matches	34;	Conservative 19;	Mismatches 36;	Indels 28; Gaps 7
QY	7 FOKGHL-----TNRDVCNNIL-STNLF--HCKDKNFIYSRPEVPAICKGIASIKV 58			
DB	8 FQRGHDSGSPSTNPVNCAMMKSAMNTGRCKPVNFFVHEPLADVQAVC----FQKNV 63			
QY	59 -----LTSEFPIIDCVNISR----PCKTKLKSKSTTFCTYCTGEO--APHP 99			
DB	64 PCKNGQSNCEYSTSNMHTDRLTSNSKFPDCLVRYTSGSEKSIIVACBGNPVYPVHF 120			

Search completed: January 22, 2004, 12:02:09
Job time : 7.29213 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 22, 2004, 12:01:21 : Search time 25.9551 Seconds

(without alignment)
1043.940 Million cell updates/sec

Title: US-09-622-613c-8

Perfect score: 580

Sequence: 1 MQDWLTFQKHLNTRDVC.....TFCVTCENQAPVHFGVGHIC 105

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_23:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	566	97.6	127	13	Q918V8
2	544	93.8	127	13	Q8UUV5
3	392.5	67.7	129	13	Q9DFI6
4	374	64.5	128	13	Q9DFY8
5	299	51.6	128	13	Q9DFY7
6	297	51.2	128	13	Q9DFY5
7	286	49.3	133	13	Q9DSM0
8	280	48.3	133	13	Q9PMR7
9	274	47.2	133	13	Q98S19
10	273	47.1	132	13	Q98SM2
11	270	46.6	133	13	Q98SL8
12	268	46.2	132	13	Q98SM1
13	263.5	45.4	132	13	Q9DF78
14	152.5	26.3	169	13	Q9W738
15	125	21.6	157	11	Q9JKI9
16	124	21.4	157	11	Q9JKJ3

17	123	21.2	152	11	Q9JKI5	Q9JKI5 mus saxicol
18	123	21.2	157	11	Q9JKJ4	Q9JKJ4 meriones un
19	120.5	20.8	153	11	Q9JKI7	Q9JKI7 mus saxicol
20	120	20.7	157	11	Q9JKJ1	Q9JKJ1 meriones un
21	119	20.5	157	11	Q9JKJ2	Q9JKJ2 meriones un
22	117	20.2	154	11	Q9JKI8	Q9JKI8 mus saxicol
23	114.5	19.7	155	11	Q9JKI9	Q9JKI9 mus pahari
24	113.5	19.6	155	11	Q9JKI3	Q9JKI3 mus saxicol
25	111.5	19.2	132	6	Q9TV24	Q9TV24 galego mohe
26	111.5	19.2	155	11	Q9JKI8	Q9JKI8 mus pahari
27	110.5	19.1	155	11	Q9JKI6	Q9JKI6 mus saxicol
28	109.5	18.9	132	6	Q9TV25	Q9TV25 eulemur ful
29	109.5	18.9	155	11	Q9JKI2	Q9JKI2 mus saxicol
30	109.5	18.9	155	11	Q9JKI4	Q9JKI4 mus saxicol
31	108.5	18.7	170	6	Q9BEC1	Q9BEC1 tregulus ja
32	108	18.6	156	11	Q9JKG6	Q9JKG6 mus caroli
33	108	18.6	156	11	Q9JKI7	Q9JKI7 mus caroli
34	107.5	18.5	119	6	Q9TV32	Q9TV32 gorilla gor
35	107.5	18.5	147	6	Q9H200	Q9H200 pan troglod
36	107.5	18.5	155	11	Q9RI34	Q9RI34 ratius nov
37	107.5	18.5	155	11	Q9RI25	Q9RI25 mus musculu
38	107	18.4	156	11	Q9VHS0	Q9VHS0 mus musculu
39	107	18.4	156	11	Q9JKG7	Q9JKG7 mus caroli
40	106.5	18.4	119	6	Q9TS06	Q9TS06 cercopithec
41	106.5	18.4	119	6	Q9TV30	Q9TV30 saginus oe
42	106	18.3	124	6	Q9TSF2	Q9TSF2 bos taurus
43	106	18.3	156	11	Q9JKH4	Q9JKH4 mus caroli
44	106	18.3	156	11	Q9JKG9	Q9JKG9 mus caroli
45	106	18.3	156	11	Q9JKH5	Q9JKH5 mus caroli

ALIGNMENTS

RESULT 1

Q918V8 PRELIMINARY: PRT: 127 AA.

AC Q918V8: 01-OCT-2000 (TREMBLrel. 15, Created)

DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)

DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)

DE Onconase variant rapLRL precursor.

OS Rana pipiens (Northern leopard frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Rana.

OX NCBI_TaxID=8404;

RN (1)

RP SEQUENCE FROM N.A.

RC TISSUE=Liver;

RX MEDLINE=20330357; PubMed=10871370;

RA Chen S.-L., Le S.-Y., Newton D.L., Maizel J.V. Jr., Rybak S.M.;

RT "A gender-specific mRNA encoding a cytotoxic ribonuclease contains a

RT 3' UTR of unusual length and structure."

RL Nucleic Acids Res. 28:2375-2382(2000).

DR EMBL: AF165133; AAF76935.1; -.

DR HSSP: P22069; IOWC.

DR InterPro: IPR001427; RNaseA.

DR Pfam: PF00074; RNaseA.1.

DR ProDom: PD000535; RNaseA.1.

DR SMART: SM00092; RNase Pc.1.

DR PROSITE: PS00127; RNASE_PANCREATIC.1.

KW Signal.

FT SIGNAL. 1 23 POTENTIAL.

FT SEQUENCE 127 AA; 14491 MW; B8511DC5407AB69B CRC64;

Query Match 97.6%, Score 566; DB 13; Length 127;

Best Local Similarity 98.1%; Pred. No. 2e-56;

Matches 102; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Q9 2 QDWLTFQKHLNTRDVCNNILSTNLFKCKDKTFTYSRREPVKAICKGIASKNVLT 61

DB 24 QDWLTFQKHLNTRDVCNNIMSTNLFKCKDKTFTYSRREPVKAICKGIASKNVLT 83

ID Q9DFY7 PRELIMINARY; PRT; 128 AA.
AC Q9DFY7;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE RC-RNase3 ribonuclease precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=20512555; PubMed=11058105;
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RT "Purification and cloning of cytotoxic ribonucleases from Rana
RT catesbeiana (bullfrog).";
RL Nucleic Acids Res. 28:4097-4104(2000).
DR EMBL; AF242554; AAG31440.2; -;
DR HSSP; P22069; 10NC.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; RNaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW SIGNAL.
FT CHAIN 1 23 POTENTIAL.
FT SIGNAL 24 128 RC-RNase3 RIBONUCLEASE.
SQ SEQUENCE 128 AA; 14517 MW; 2B14986082E0587D CRC64;

Query Match 51.6%; Score 299; DB 13; Length 128;
Best Local Similarity 52.9%; Pred. No. 3.7e-26;
Matches 55; Conservative 13; Mismatches 36; Indels 0; Gaps 0;

QY 2 QDWLTFQKKHLTNRDVCNNILSTNLFHCKDKNTFIYSRPPVKAICKGIASKNVLT 61
DB 24 QDWTFQKKHLTDRKKVCDVEMKALFDCKKTNTFIARPRVQALCKNIKNTNVL 83

QY 62 SEFYLSDCNVTSPCKYKLLKSTITFCVTCENQAPVHFVGVC 105
DB 84 DAFLLPQCDRIKLPCHYKLSSTNTICITCVNQLPIHFAGVGC 127

RESULT 6
ID Q9DFY5 PRELIMINARY; PRT; 128 AA.
AC Q9DFY5;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE RC-RNase6 ribonuclease precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=20512555; PubMed=11058105;
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RT "Purification and cloning of cytotoxic ribonucleases from Rana
RT catesbeiana (bullfrog).";
RL Nucleic Acids Res. 28:4097-4104(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=20512555; PubMed=11058105;
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF242556; AAG31442.2; -;
DR HSSP; P22069; 10NC.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; RNaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.

KW SIGNAL. 1 23 POTENTIAL.
FT CHAIN 24 128 RC-RNase6 RIBONUCLEASE.
SQ SEQUENCE 128 AA; 14804 MW; AFBFB67D266C7C2 CRC64;

Query Match 51.2%; Score 297; DB 13; Length 128;
Best Local Similarity 51.9%; Pred. No. 6.2e-26;
Matches 54; Conservative 14; Mismatches 36; Indels 0; Gaps 0;

QY 2 QDWLTFQKKHLTNRDVCNNILSTNLFHCKDKNTFIYSRPPVKAICKGIASKNVLT 61
DB 24 QDWTFQKKHLTDRKKVCDVEMKALFDCKKTNTFIARPRVQALCKNIKNTNVL 83

QY 62 SEFYLSDCNVTSPCKYKLLKSTITFCVTCENQAPVHFVGVC 105
DB 84 DVFYLPQCNRRKKLPCHYRLDGSNTICLTCKMELPIHFAGVGC 127

RESULT 7
ID Q98SM0 PRELIMINARY; PRT; 133 AA.
AC Q98SM0;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE RNase A-type ribonuclease rc208 precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21539506; PubMed=11683320;
RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT "Rapid diversification of RNase A superfamily ribonuclease from the
RT bullfrog, Rana catesbeiana.";
RL J. Mol. Evol. 53:31-38(2001).
DR EMBL; AF351209; AAK30255.1; -;
DR HSSP; P11916; 1BC4.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; RNaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_PC; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW SIGNAL.
FT SIGNAL. 1 22 POTENTIAL.
FT SIGNAL 133 AA; 14628 MW; 87FCF122C3499E02 CRC64;

Query Match 49.3%; Score 286; DB 13; Length 133;
Best Local Similarity 47.7%; Pred. No. 1.1e-24;
Matches 53; Conservative 17; Mismatches 33; Indels 8; Gaps 3;

QY 2 QDWLTFQKKHLTNRDVCNNILSTNLF----HCKDKNTFIYSRPPVKAICKGIASKN 57
DB 23 QNWATFOQKHITNTSSINCNTIMDNIIYIVGQCKGVNTFISSATTVKAICTGVI-NMN 81

QY 58 VLTTSSEFVLSDC--NVTSRCKYKLLKSTITFCVTCENQAPVHFVGVC 105
DB 82 VLSITRQLNTCTRTSITPFCPSSTENNYICVKCENQVPHFAGVGC 132

RESULT 8
ID Q9PWR7 PRELIMINARY; PRT; 133 AA.
AC Q9PWR7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Ribonuclease precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.

```

OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=98165025; PubMed=9497370;
RA Huang H.C., Wang S.C., Leu Y.J., Lu S.C., Liao Y.D.;
RT "The Rana catesbeiana rcr gene encoding a cytotoxic ribonuclease.
RT Tissue distribution, cloning, purification, cytotoxicity, and active
RT residues for RNase activity.";
RL J. Biol. Chem. 273:6395-6401(1998).
DR EMBL; AF039104; AAD10702.1; -.
DR HSSP; P11916; 1BC4.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_PC; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL.
FT CHAIN.
SQ SEQUENCE 133 AA; 14762 MW; A7D62594F7D16F0C CRC64;

Query Match 48.3%; Score 280; DB 13; Length 133;
Best Local Similarity 47.7%; Pred. No. 5.4e-24;
Matches 53; Conservative 17; Mismatches 33; Indels 8; Gaps 3;

OY 2 QWLTFOKHLNTRDVCNNILSTNLF----HCKDKNTFIYSRPPVKAICKGIASKN 57
DB 23 QNWATFQKHHTNTPINCTIMDNNIYIVGGCKRVNTFISSATTVKAICTGVI-NMN 81

OY 58 VLTTFSEFYLSDC---NVTSRPCKYKLKSKTITFCVTCENQAPVHFVGVGHC 105
DB 82 VLSTTRFQLNTRTTSITRPPCPYSSRTETNYICVKCENQYPVHFAGIGRC 132

RESULT 9
Q98SL9 ID Q98SL9 PRELIMINARY; PRT; 133 AA.
AC Q98SL9;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE RNase A-type ribonuclease rc212 precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21539506; PubMed=11683320;
RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT "Rapid diversification of RNase A superfamily ribonuclease from the
RT bullfrog, Rana catesbeiana.";
RL J. Mol. Evol. 53:31-38(2001).
DR HSSP; P11916; 1BC4.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_PC; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL.
FT CHAIN.
SQ SEQUENCE 133 AA; 14615 MW; C8785B236B26E54E CRC64;

Query Match 47.2%; Score 274; DB 13; Length 133;
Best Local Similarity 45.9%; Pred. No. 2.6e-23;
Matches 51; Conservative 18; Mismatches 34; Indels 8; Gaps 3;

OY 2 QWLTFOKHLNTRDVCNNILSTNLF----HCKDKNTFIYSRPPVKAICKGIASKN 57
DB 23 QNWATFQKHHTNTPINCTIMDNNIYIVGGCKRVNTFISSATTVKAICTGVI-NMN 81

OY 58 VLTTFSEFYLSDC---NVTSRPCKYKLKSKTITFCVTCENQAPVHFVGVGHC 105
DB 82 VLSTTRFQLNTRTTSITRPPCPYSSRTETNYICVKCENQYPVHFAGIGRC 132

RESULT 9
Q98SL9 ID Q98SL9 PRELIMINARY; PRT; 133 AA.
AC Q98SL9;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE RNase A-type ribonuclease rc212 precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21539506; PubMed=11683320;
RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT "Rapid diversification of RNase A superfamily ribonuclease from the
RT bullfrog, Rana catesbeiana.";
RL J. Mol. Evol. 53:31-38(2001).
DR EMBL; AF351210; AAK30256.1; -.
DR HSSP; P11916; 1BC4.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_PC; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL.
FT CHAIN.
SQ SEQUENCE 133 AA; 14615 MW; C8785B236B26E54E CRC64;

Query Match 47.1%; Score 273; DB 13; Length 132;
Best Local Similarity 45.9%; Pred. No. 3.3e-23;
Matches 51; Conservative 15; Mismatches 37; Indels 8; Gaps 3;

OY 2 QWLTFOKHLNTRDVCNNILSTNLF----HCKDKNTFIYSRPPVKAICKGIASKN 57
DB 23 QWAKFQKHIPSTSSINCNTIMDNNIYIVGGCKRVNTFISSATTVKAICNG-VTNSN 81

OY 58 VLTTFSEFYLSDC---NVTSRPCKYKLKSKTITFCVTCENQAPVHFVGVGHC 105
DB 82 VLSTTRFQLNTRTTSITRPPCPYSSRTETNYICVKCENQYPVHFAGIGRC 132

RESULT 11
Q98SL8 ID Q98SL8 PRELIMINARY; PRT; 133 AA.
AC Q98SL8;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE RNase A-type ribonuclease rc218 precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21539506; PubMed=11683320;
RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT "Rapid diversification of RNase A superfamily ribonuclease from the
RT bullfrog, Rana catesbeiana.";
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RL J. Mol. Evol. 53:31-38(2001).
DR EMBL; AF351211; AAK30257.1; -.
DR HSSP; P11916; 18C4.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW SIGNAL.
FT SIGNAL.
SQ SEQUENCE 133 AA; 14590 MW; 8B40B9A94FASB943 CRC64;

Query Match 46.6%; Score 270; DB 13; Length 133;
Best Local Similarity 45.0%; Pred. No. 7.4e-23;
Matches 50; Conservative 19; Mismatches 34; Indels 8; Gaps 3;

Qy 2 QDWLTFOKHULTNTRDVCNNILSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 57
Db 23 QNWAATFOQHITNTSSINCNSIMNSLYIVGQCKKNTFIASSATTVKIGICSG-VTDKK 81

Qy 58 VLTSEFYLSDCN---VTSRPPCKYKLLKSTITFCVTCENQAPVHFVGVGHC 105
Db 82 VLSSTKFOLDICTRIFITPRPCPSSTRTETNYICVKCENQYVHFVAGIGQC 132

RESULT 12
Q98SM1 ID Q98SM1 PRELIMINARY; PRT; 132 AA.
AC Q98SM1.
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE RNase A-type ribonuclease rc204 precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=21539506; PubMed=11683320;
RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT "Rapid diversification of RNase A superfamily ribonuclease from the
RT bullfrog, Rana catesbeiana."
RL J. Mol. Evol. 53:31-38(2001).
DR EMBL; AF351208; AAK30254.1; -.
DR HSSP; P11916; 18C4.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW SIGNAL.
FT SIGNAL.
SQ SEQUENCE 132 AA; 14704 MW; 95D61760F729868E CRC64;

Query Match 46.2%; Score 268; DB 13; Length 132;
Best Local Similarity 46.8%; Pred. No. 1.2e-22;
Matches 52; Conservative 15; Mismatches 36; Indels 8; Gaps 3;

Qy 2 QDWLTFOKHULTNTRDVCNNILSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 57
Db 23 QDWPTFOKHULTSSIDCNDIMDKIYIVRGQCKKNTFIYSATTVAICTGVLSN-N 81

Qy 58 VLTSEFYLSDCN---VTSRPPCKYKLLKSTITFCVTCENQAPVHFVGVGHC 105
Db 82 VLSSTRQLXXXTFTITSRPPCVSSSTKETNKICVKCENQYVHFVAGIGKC 132

RESULT 13
Q9DF78 ID Q9DF78 PRELIMINARY; PRT; 132 AA.
AC Q9DF78.
DT 01-MAR-2001 (TrEMBLrel. 16, Created)

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DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE RC-RNaseL1 ribonuclease precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RN SEQUENCE FROM N.A.
RX TISSUE=Liver;
RX MEDLINE=20512555; PubMed=11058105;
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RT "Purification and cloning of cytotoxic ribonucleases from Rana
RT catesbeiana (bullfrog).";
RL Nucleic Acids Res. 28:4097-4104(2000).
RN [2]
RN SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF288642; AAG30414.2; -.
DR HSSP; P11916; 18C4.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW SIGNAL.
FT SIGNAL.
FT CHAIN 1 21 POTENTIAL.
FT CHAIN 22 132 RC-RNASEL1 RIBONUCLEASE.
SQ SEQUENCE 132 AA; 14625 MW; DBD9A517452PBE53 CRC64;

Query Match 45.4%; Score 263.5; DB 13; Length 132;
Best Local Similarity 42.3%; Pred. No. 4e-22;
Matches 47; Conservative 20; Mismatches 37; Indels 7; Gaps 2;

Qy 2 QDWLTFOKHULTNTRDVCNNILSTNLF----HCKDKNTFIYSRPEPVKAICKGIIASKN 57
Db 22 QNWAFFKEKHITSTSSIDCNDIMDKIYIVGKCKERTFIISSEDNVKALCSGVSPDRK 81

Qy 58 VLTSEFYLSDC---NVTSPCKYKLLKSTITFCVTCENQAPVHFVGVGHC 105
Db 82 ELSTTSFKLNTCIRDSITPRPCPYHPSPNNKICVKCEKQLPVHFVGVGKC 132

RESULT 14
Q9W738 ID Q9W738 PRELIMINARY; PRT; 169 AA.
AC Q9W738.
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE FRU2 protein.
GN FRU2.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=96069863; PubMed=7585965;
RA Kinoshita N., Minshall J., Kirschner M.W.;
RT "The identification of two novel ligands of the FGF receptor by a
RT yeast screening method and their activity in Xenopus development.";
RL Cell 83:621-630(1995).
RN [2]
RN SEQUENCE FROM N.A.
RA Kinoshita N., Kirschner M.W.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF159166; AAD41901.1; -.
DR HSSP; P00656; 1LSQ.
DR InterPro; IPR001427; RNaseA.

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DR Pfam; PF00074; rnaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
SQ SEQUENCE 169 AA; 18891 MW; D969F3E43B3CE1B8 CRC64;

Query Match      26.3%; Score 152.5; DB 13; Length 169;
Best Local Similarity 36.1%; Pred. No. 1.9e-09;
Matches 39; Conservative 19; Mismatches 35; Indels 15; Gaps 6;

QY 7 FOKHLLTNT-RDVCN-----NILSTNLFHCKDKNTFY-SRPEPVKAICKGIIASKNV 58
DB 33 FWEKHIVKEGAETNCNQTIKDRNIRFKN--NCKFRNTFIHDTNGKKVKEMCAGIVKSTFV 90
QY 59 LTTSEFYLSDCNV---TSRP--CKYKLKXSTITFCVTCENQAPVHVG 101
DB 91 ISKELLPLTDCLLMGRTARPNCAYNQTRTGTGVTINICENNYPVHFAG 138

RESULT 15
Q9JKI9 PRELIMINARY; PRT; 157 AA.
AC Q9JKI9;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE 01-NAR-2003 (TREMBLrel. 23, Last annotation update)
DE Eosinophil-associated ribonuclease 44.
GN EAR44.
OS Meriones unguiculatus (Mongolian jird) (Mongolian gerbil).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;
OC Meriones.
OX NCBI_TaxID=10047;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20243759; PubMed=10758160;
RA Zhang J., Dyer K.D., Rosenberg H.F.;
RT "Evolution of the rodent eosinophil-associated ribonuclease gene
RT family by rapid gene sorting and positive selection.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:4701-4706(2000).
DR EMBL; AF238394; AAF67694.1; -.
DR HSSP; P10153; 1HI2.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNASE_PC; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
SQ SEQUENCE 157 AA; 17887 MW; 34FE2AE777FEF3709 CRC64;

Query Match      21.6%; Score 125; DB 11; Length 157;
Best Local Similarity 30.3%; Pred. No. 2.4e-06;
Matches 33; Conservative 21; Mismatches 35; Indels 20; Gaps 7;

QY 4 WLTFQKHLLTNRDVCN-NILSTNLF--HCKDKNTFYSRPEPV-----KAICKGII 53
DB 36 WFTIQ--HISNTTTTCNAAMLGVANNYTGRCXDLNLTFLHTRFANYVNECYNNTTCKN-- 91
QY 54 ASKNVL-TTSEFYLSDCNVTS-----RPCKYKLKXSTITFCVTCENQAP 96
DB 92 GRNCHDSRSKVSITDCNLTSPSANYRQCYORTARKEYRIACNKTTP 140
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Search completed: January 22, 2004, 12:08:51
Job time : 26.9551 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: January 22, 2004, 12:01:20 ; Search time 6.65169 Seconds
(without alignments)
784.758 Million cell updates/sec

Title: US-09-622-613c-17
Perfect score: 607
Sequence: 1 MOWATFOQKHINTPIICN.....ICVKCNQYVHFAGIGRCP 111

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	591.5	97.4	111	1 RNP0_RANCA	P11916 rana cateeb
2	455	75.0	111	1 LECS_RANCA	P18039 rana japoni
3	374	61.6	111	1 RNP1_RANCA	P14626 rana cateeb
4	277.5	45.7	104	1 RNP30_RANPI	P22069 rana pipien
5	154.5	25.5	145	1 ANG3_MOUSE	P97802 mus musculus
6	149.5	24.6	145	1 ANGR_MOUSE	Q64438 mus musculus
7	135.5	22.3	124	1 RNP_BALAC	P00673 balaenopter
8	135.5	22.3	145	1 ANGI_MOUSE	P21570 mus musculus
9	133.5	22.0	167	1 RNP0_BOVIN	P39873 bos taurus
10	132.5	21.8	124	1 RNP_PIG	P00671 sus scrofa
11	131.5	21.7	119	1 RNP_IGUIG	P80287 iguana igua
12	128.5	21.2	151	1 RNP0_CAPCA	P79351 capreolus c
13	127.5	21.0	123	1 ANG2_BOVIN	P80929 bos taurus
14	127.5	21.0	141	1 RNP0_GIRCA	Q29542 giraffa cam
15	127.5	21.0	151	1 RNP0_AXIPR	P87350 axis porcin
16	125	20.6	146	1 ANGI_SAISS	Q8wn60 saimiri sci
17	124	20.4	146	1 ANGI_MIOTA	Q8wn65 miopithecus
18	123.5	20.3	143	1 RNP0_SHEEP	Q29543 ovis aries
19	122.5	20.2	124	1 RNP0_ANTAM	P00668 antilocapra
20	122.5	20.2	146	1 ANGI_CERAB	Q8wn66 cercopithec
21	122	20.1	122	1 RNP0_MACRO	P00686 macropus r
22	120.5	19.9	128	1 RNP0_MYOCO	P00676 myocastor c
23	120.5	19.9	149	1 RNP0_MOUSE	P00683 mus musculus
24	120.5	19.8	146	1 ANGI_AOTTR	Q8wn61 aotus trivi
25	120	19.8	147	1 ANGI_PONPY	Q8wn67 pongo pygma
26	119.5	19.7	123	1 ANGI_PIG	P31346 sus scrofa
27	118.5	19.5	128	1 RNP0_CAVPO	P00679 cavia porce
28	118	19.4	146	1 ANGI_SAGOE	Q8wn62 saguinus oe
29	117.5	19.4	128	1 RNP0_HORSE	P00674 equus caball
30	116.5	19.2	124	1 RNP0_CAMDR	P00670 camelus dro
31	116.5	19.2	128	1 RNP0_PROGU	P04059 proechimys
32	115.5	19.0	146	1 ANGI_MACMU	Q8wn63 macaca mula
33	114	18.8	148	1 ANGI_BOVIN	P10152 bos taurus

ALIGNMENTS

RESULT 1

ID	RNP0_RANCA	STANDARD;	PRT;	111 AA.
AC	P11916;			
DT	01-OCT-1989 (Rel. 12, Created)			
DT	01-FEB-1994 (Rel. 28, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	Ribonuclease, oocytes (EC 3.1.27.-) (RC-RNase)			(Sialic acid-binding
DE	lectin) (SBL-C)			
OS	Rana catesbeiana (Bull frog).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.			
OX	NCBI_TaxID=8400;			
RN	[1]			
RP	SEQUENCE.			
RC	TISSUE=Egg;			
EX	MEDLINE=87299649; PubMed=3304421;			
RA	Titani K., Takio K., Kuwada M., Nitta K., Sakakibara F., Kawauchi H.,			
RA	Takayanagi G., Hakomori S.;			
RT	"Amino acid sequence of sialic acid binding lectin from frog (Rana			
RT	catesbeiana) eggs."			
RT	Biochemistry 26:2189-2194(1987).			
RL	[2]			
RP	CHARACTERIZATION, AND SEQUENCE OF 59-79.			
RX	MEDLINE=92220613; PubMed=1373237;			
RA	Liao Y.-D.;			
RT	"A pyrimidine-guanine sequence-specific ribonuclease from Rana			
RT	catesbeiana (bullfrog) oocytes."			
RL	Nucleic Acids Res. 20:1371-1377(1992).			
RN	[3]			
RP	CHARACTERIZATION.			
RC	TISSUE=Egg;			
RX	MEDLINE=93192604; PubMed=8448385;			
RA	Nitta K., Oyama F., Oyama R., Sekiguchi K., Kawauchi H.,			
RA	Takayanagi Y., Hakomori S., Titani K.;			
RT	"Ribonuclease activity of sialic acid-binding lectin from Rana			
RT	catesbeiana eggs."			
RL	Glycobiology 3:37-45(1993).			
RN	[4]			
RP	STRUCTURE BY NMR.			
RX	MEDLINE=98437383; PubMed=9761686;			
RA	Chang C.-F., Chen C., Chen Y.-C., Hom K., Huang R.-F., Huang T.H.;			
RT	"The solution structure of a cytotoxic ribonuclease from the oocytes			
RT	of Rana catesbeiana (bullfrog)."			
RL	J. Mol. Biol. 283:231-244(1998).			
CC	-I- FUNCTION: Preferentially cleaves single-stranded RNA at pyrimidine			
CC	residues with a 3'flanking guanine. Hydrolyzes poly(U) and poly(C)			
CC	as substrates, and prefers the former. The S-lectins in frog eggs			
CC	may be involved in the fertilization and development of the frog			
CC	embryo. This lectin agglutinates various animal cells, including			
CC	normal lymphocytes, erythrocytes, and fibroblasts of animal and			
CC	human origin.			
CC	-I- SUBUNIT: Monomer.			
CC	-I- SUBCELLULAR LOCATION: Secreted.			
CC	-I- SIMILARITY: Belongs to the pancreatic ribonuclease family.			
DR	PIR; A27121; A27121.			

34	113.5	18.7	124	1 RNP_RANTA	P00666 rangifer ta
35	113.5	18.7	146	1 ANGI_PAPHA	Q8wn64 papio hamad
36	113	18.6	147	1 ANGI_HUMAN	P03950 homo sapien
37	113	18.6	147	1 ANGI_PANTR	Q8wn68 pan troglod
38	112.5	18.5	124	1 RNP_CAPCA	P00664 capreolus c
39	112.5	18.5	124	1 RNP_GIRCA	P00662 giraffa cam
40	112.5	18.5	148	1 RNS4_MOUSE	Q9jjh1 mus musculus
41	112	18.5	125	1 ANGI_RABIT	P31347 oryctolagus
42	111.5	18.4	130	1 RNP_CRILO	P24717 cricetus
43	111.5	18.4	147	1 RNS4_RAT	O55004 rattus norv
44	111.5	18.4	149	1 RNP_ACOCA	Q9wt55 acomys cahi
45	110.5	18.2	124	1 RNP_AEPME	P07847 aepyceros m

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DR PDB; 1BC4; 28-OCT-98.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; RNaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase PC; 1.
DR PROSITE; PS00127; RNASE PANCREATIC; 1.
DR Hydrolase; Nuclease; Endonuclease; Sialic acid; Lectin; 3D-structure;
KW Pyrrolidone carboxylic acid. PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 1 1
FT ACT_SITE 10 10
FT ACT_SITE 35 35
FT ACT_SITE 103 103
FT DISULFID 19 71
FT DISULFID 34 81
FT DISULFID 52 96
FT DISULFID 93 110
FT HELIX 3 10
FT HELIX 19 23
FT TURN 26 27
FT STRAND 37 41
FT HELIX 45 51
FT TURN 52 52
FT STRAND 57 62
FT STRAND 68 73
FT STRAND 83 88
FT STRAND 92 97
FT TURN 98 99
FT STRAND 100 107
FT SEQUENCE 111 AA; 12464 MW; 0BC9E5F5729ECF4 CRC64;

Query Match 97.4%; Score 591.5; DB 1; Length 111;
Best Local Similarity 99.1%; Pred. No. 3.8e-57;
Matches 110; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

OY 2 QNWATFQQRHIIPTPII-CNTIMDNNIYVGGCKRVNTFISSATTVKAICTGVINMV 60
DB 1 QNWATFQQRHIIPTPII-CNTIMDNNIYVGGCKRVNTFISSATTVKAICTGVINMV 60
OY 61 LSTTRFQNLCTRTSITPRCPYSSRTETNYICVKCENQYPVHFAGIRCP 111
DB 61 LSTTRFQNLCTRTSITPRCPYSSRTETNYICVKCENQYPVHFAGIRCP 111

RESULT 2
LECS_RANJA STANDARD; PRT; 111 AA.
AC P18839;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Sialic acid-binding lectin (EC 3.1.27.-).
OS Rana japonica (Japanese redbellied frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8402;
RN [1]
RP SEQUENCE
RC TISSUE=Egg;
RX MEDLINE=91035319; PubMed=2229005;
RA Kamiya Y., Oyama F., Oyama R., Sakakibara F., Nitta K., Kawauchi H.,
RA Takayanagi Y., Titani K.;
RT "Amino acid sequence of a lectin from Japanese frog (Rana japonica)
RT eggs.";
RL J. Biochem. 108:139-143 (1990).
CC -1- FUNCTION: THE S-LECTINS IN FROG EGGS MAY BE INVOLVED IN THE
CC FERTILIZATION AND DEVELOPMENT OF THE FROG EMBRYO. THIS LECTIN
CC PREFERENTIALLY AGGLUTININATE A LARGE VARIETY OF TUMOR CELLS, BUT IT
CC DOES NOT AGGLUTININATE NON-TRANSFORMED CELLS AND ERYTHROCYTES.
CC -1- SUBUNIT: Monomer.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the pancreatic ribonuclease family.
PIR; JX0120; JX0120.

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DR HSSP; P11916; 1BC4.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; RNaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase PC; 1.
DR PROSITE; PS00127; RNASE PANCREATIC; 1.
DR Hydrolase; Nuclease; Endonuclease; Sialic acid; Lectin;
KW Pyrrolidone carboxylic acid. PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 1 1
FT ACT_SITE 10 10
FT ACT_SITE 35 35
FT ACT_SITE 104 104
FT DISULFID 19 72
FT DISULFID 34 82
FT DISULFID 52 97
FT DISULFID 94 111
FT SEQUENCE 111 AA; 12326 MW; FDEBDDF3834ED679 CRC64;

Query Match 75.0%; Score 455; DB 1; Length 111;
Best Local Similarity 78.4%; Pred. No. 2.1e-42;
Matches 87; Conservative 7; Mismatches 15; Indels 2; Gaps 2;

OY 2 QNWATFQQRHIIPTPII-CNTIMDNNIYVGGCKRVNTFISSATTVKAICTGV-INNM 59
DB 1 QNWATFQQRHIIPTPII-CNTIMDNNIYVGGCKRVNTFISSATTVKAICTGV-INNM 59
OY 60 VLSTTRFQNLCTRTSITPRCPYSSRTETNYICVKCENQYPVHFAGIRCP 110
DB 61 VLSTTRFQNLCTRTSITPRCPYSSRTETNYICVKCENQYPVHFAGIRCP 111

RESULT 3
RNPL_RANCA STANDARD; PRT; 111 AA.
AC P14626;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ribonuclease, liver (EC 3.1.27.5).
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE
RC TISSUE=Liver;
RX MEDLINE=90130374; PubMed=2613682;
RA Nitta R., Katayama N., Okabe Y., Iwama M., Watanabe H., Abe Y.,
RA Okazaki T., Ohgi K., Irie M.;
RT "Primary structure of a ribonuclease from bullfrog (Rana catesbeiana)
RT liver.";
RL J. Biochem. 106:729-735 (1989).
CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
CC phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
CC with 2',3'-cyclic phosphate intermediates.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the pancreatic ribonuclease family.
PIR; JX0085; JX0085.
DR HSSP; P11916; 1BC4.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; RNaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase PC; 1.
DR PROSITE; PS00127; RNASE PANCREATIC; 1.
DR Hydrolase; Nuclease; Endonuclease; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1
FT ACT_SITE 10 10
FT ACT_SITE 35 35
FT ACT_SITE 104 104
FT DISULFID 19 72
FT DISULFID 34 82
FT DISULFID 52 97
FT DISULFID 94 111
FT SEQUENCE 111 AA; 12326 MW; FDEBDDF3834ED679 CRC64;

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[illegible]

QY 7 FOOKHII-----NTPIICNTIMNNIYVGGCKRVNTFIISSTATTVAICTGVNNV 60
 Db 8 FORQHWDGNSGPNPNYCNQMMRR-KYTGCRCKPVNTFVHESLEDYKAVCS---QKXV 63
 QY 61 L-----STTRFQNTCTRTSITPRP-CPYSSRTETNYCVKCE-NQY-PVHF 104
 Db 64 LCKNGRTNYESNSTMHTDCRTGSSKYPNCAYKTSQEKHIIIVACEGPNVPVPHF 120

RESULT 8

ANGI_MOUSE STANDARD; PRT; 145 AA.
 AC P21570;
 DT 01-MAY-1991 (Rel. 18, Created)
 DT 01-MAY-1991 (Rel. 18, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Angiogenin precursor (EC 3.1.27.-) (Ribonuclease 5) (RNase 5).
 GN ANG.

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE=91025023; PubMed=2222458;
 RA Bond M.D., Vallee B.L.;
 RT "Isolation and sequencing of mouse angiogenin DNA.";
 RL Biochem. Biophys. Res. Commun. 171:988-995(1990).
 RN [2]

RP PARTIAL SEQUENCE.
 RC TISSUE=Serum;
 RX MEDLINE=93192291; PubMed=8448182;
 RA Bond M.D., Strydom D.J., Vallee B.L.;
 RT "Characterization and sequencing of rabbit, pig and mouse
 RT angiogenins: discernment of functionally important residues and
 RT regions.";
 RL Biochem. Biophys. Acta 1162:177-186(1993).

CC -!- FUNCTION: MAY FUNCTION AS A TRNA-SPECIFIC RIBONUCLEASE THAT BINDS
 CC TO ACTIN ON THE SURFACE OF ENDOTHELIAL CELLS; ONCE BOUND,
 CC ANGIOGENIN IS ENDOCYTOSED AND TRANSLOCATED TO THE NUCLEUS, THEREBY
 CC PROMOTING THE ENDOTHELIAL INVASIVENESS NECESSARY FOR BLOOD VESSEL
 CC FORMATION. ANGIOGENIN INDUCES VASCULARIZATION OF NORMAL AND
 CC MALIGNANT TISSUES. ABOLISHES PROTEIN SYNTHESIS BY SPECIFICALLY
 CC HYDROLYZING CELLULAR TRNAS.
 CC -!- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
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 CC or send an email to license@isb-sib.ch).

CC EMBL; U22516; AAA91366.1; --
 CC PIR; A35932; A35932.
 CC HSSP; P03950; 1A4Y.
 CC MGD; MGI:88022; Ang.
 CC InterPro; IPR001427; RNaseA.
 CC Pfam; PF00074; RNaseA; 1.
 CC PRINTS; PR00794; RIBONUCLEASE.
 CC ProDom; PD000535; RNaseA; 1.
 CC SMART; SM00092; RNaseA; 1.
 CC PROSITE; PS00127; RNASE PANCREATIC; 1.
 CC Hydrolase; Nuclease; Endonuclease; Angiogenesis;
 CC Protein synthesis inhibitor; Signal; Pyrrolidone carboxylic acid.
 FT SIGNAL 1 24
 FT CHAIN 25 145 ANGIOGENIN.
 FT MOD_RES 25 25 PYRROLIDONE CARBOXYLIC ACID (BY
 FT PIR; S20066; S20066.
 FT ACT_SITE 37 37 BY SIMILARITY.

FT ACT_SITE 64 64 BY SIMILARITY.
 FT ACT_SITE 137 137 BY SIMILARITY.
 FT DISULFID 50 104 BY SIMILARITY.
 FT DISULFID 63 115 BY SIMILARITY.
 FT DISULFID 81 130 BY SIMILARITY.
 SQ SEQUENCE 145 AA; 16228 MW; 069442608B764938 CRC64;
 Query Match 22.3%; Score 135.5; DB 1; Length 145;
 Best Local Similarity 39.5%; Pred. No. 9e-08; 29; Indels 5; Gaps 3;
 Matches 30; Conservative 12; Mismatches 12;
 QY 34 CKRVNTFIISSTATTVAICT---TGVINNV-LSTTRFQNTCTRTSITPR-PCPYSSRTE 88
 Db 63 CKDVNTFIHGNSNIKAICGANGSPYRENLRMSKSPFQVTTCKTGSGSPRPCCQYRASG 122
 QY 89 TNYICVKCENQYVPHF 104
 Db 123 FRHVVIACENGLPVHF 138

RESULT 9

RNR_BOVIN STANDARD; PRT; 167 AA.
 ID RNR_BOVIN
 AC P39873;

DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Ribonuclease, brain precursor (EC 3.1.27.-) (BRB).
 GN BRN.

OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92093604; PubMed=1754384;
 RA Sasso M.P., Carsana A., Confalone E., Cosi C., Sorrentino S.,
 RA Viola M., Palmieri M., Russo E., Furia A.;
 RT "Molecular cloning of the gene encoding the bovine brain ribonuclease
 RT and its expression in different regions of the brain.";
 RL Nucleic Acids Res. 19:6469-6474(1991).
 RN [2]

RP SEQUENCE OF 27-167, AND CARBOHYDRATE-LINKAGE SITES.

RC TISSUE=Brain;
 RX MEDLINE=89214015; PubMed=3243767;
 RA Watanabe H., Katoh H., Ishii M., Komoda Y., Sanda A., Takizawa Y.,
 RA Ohgi K., Irie M.;
 RT "Primary structure of a ribonuclease from bovine brain.";
 RL J. Biochem. 104:939-945(1988).
 RN [3]

RP SEQUENCE OF 27-167 FROM N.A.
 RX MEDLINE=96139017; PubMed=8587129;
 RA Confalone E., Beintema J.J., Sasso M.P., Carsana A., Palmieri M.,
 RA Vento M.T., Furia A.;
 RT "Molecular evolution of genes encoding ribonucleases in ruminant
 RT species";
 RL J. Mol. Evol. 41:850-858(1995).

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.

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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC or send an email to license@isb-sib.ch).

CC EMBL; X59767; CA42439.1; --
 CC EMBL; S81744; AAB36138.1; --
 CC PIR; S20066; S20066.
 CC HSSP; P00656; 2RNS.

```
DR GlycoSuiteDB: P39873; -.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; RNaseA; 1.
DR PRINTS: PR00794; RIBONUCLEASE.
DR ProDom: PD000535; RNaseA; 1.
DR SMART: SM00092; RNase P; 1.
DR PROSITE: PS00127; RNASE_PANCREATIC; 1.
KW Hydrolase; Nuclease; Endonuclease; Glycoprotein; Signal.
FT SIGNAL 1 26
FT CHAIN 27 167 RIBONUCLEASE, BRAIN.
FT ACT_SITE 38 38 BY SIMILARITY.
FT ACT_SITE 67 67 BY SIMILARITY.
FT ACT_SITE 145 145 BY SIMILARITY.
FT DISULFID 52 110 BY SIMILARITY.
FT DISULFID 66 121 BY SIMILARITY.
FT DISULFID 84 136 BY SIMILARITY.
FT DISULFID 91 98 BY SIMILARITY.
FT CARBOHYD 88 88 /FTID=CAR_000005.
FT CARBOHYD 155 155 O-LINKED.
FT CARBOHYD 159 159 O-LINKED.
FT CONFLICT 155 155 T -> S (IN REF. 2).
SQ SEQUENCE 167 AA; 18450 MW; 681CAAC3CC2FC459 CRC64;

Query Match 22.0%; Score 133.5; DB 1; Length 167;
Best Local Similarity 31.4%; Pred. No. 1.7e-07;
Matches 38; Conservative 17; Mismatches 43; Indels 23; Gaps 7;

QY 5 ATFOQKHI-----INTPIICNTIMDNIIYVGGQCKRVNTFIISATTVAICTGVINM 58
DB 32 AKPRHMDSSGSSSNPNYCNQMRR-RMTHGRCKPVPNTFVHESLDVKAACS---QK 87
QY 59 NVL-----STTRFOLNTCTRTSITPRP-CPYSSRTETNYICVKCE-NOY-PVHFA 105
DB 88 NITCKGNHCNVCQSKSTMSITDCRETGSSKYPNCAYKTSQOKYITVACEGHPVPVPHFD 147
QY 106 G 106
DB 148 G 148

RESULT 10
RNP_PIG
ID RNP_PIG STANDARD; PRT; 124 AA.
AC P00671;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).
GN RNASE1 OR RNS1.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE.
RX MEDLINE=70104197; PubMed=5460946;
RA Jackson R.L., Hirs C.H.W.;
RT "The primary structure of porcine pancreatic ribonuclease. II. The amino acid sequence of the reduced S-aminoethylated protein.";
RL J. Biol. Chem. 245:637-653 (1970).
RN [2]
RP REVISION TO 2.
RA Wierenga R.K., Huizinga J.D., Gaastera W., Welling G.W., Beintema J.J.;
RT "Affinity chromatography of porcine pancreatic ribonuclease and reinvestigation of the N-terminal amino acid sequence.";
RL FEBS Lett. 31:181-185 (1973).
RN [3]
RP DISULFIDE BONDS.
RX MEDLINE=70104198; PubMed=4904878;
RA Phelan J.J., Hirs C.H.W.;
RT "The primary structure of porcine pancreatic ribonuclease. 3. The disulfide bonds.";
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RL J. Biol. Chem. 245:654-661 (1970).
CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-phosphates and 3'-phosphooligonucleotides ending in C-P or U-P with 2',3'-cyclic phosphate intermediates.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Pancreas.
CC -1- SIMILARITY: Belongs to the pancreatic ribonuclease family.
DR PIR: A92071; NRPG.
DR HSP; P00656; 1SRN.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; RNaseA; 1.
DR PRINTS: PR00794; RIBONUCLEASE.
DR ProDom: PD000535; RNaseA; 1.
DR SMART: SM00092; RNase P; 1.
DR PROSITE: PS00127; RNASE_PANCREATIC; 1.
KW Hydrolase; Nuclease; Endonuclease; Glycoprotein.
FT DISULFID 26 84
FT DISULFID 40 95
FT DISULFID 58 110
FT DISULFID 65 72
FT ACT_SITE 12 12 BY SIMILARITY.
FT ACT_SITE 41 41 BY SIMILARITY.
FT ACT_SITE 119 119 BY SIMILARITY.
FT CARBOHYD 21 21 N-LINKED (GLCNAC. .).
FT CARBOHYD 34 34 N-LINKED (GLCNAC. .).
FT CARBOHYD 76 76 N-LINKED (GLCNAC. .).
SQ SEQUENCE 124 AA; 13804 MW; 0AC28CDE14111845 CRC64;

Query Match 21.8%; Score 132.5; DB 1; Length 124;
Best Local Similarity 31.6%; Pred. No. 1.6e-07;
Matches 36; Conservative 19; Mismatches 42; Indels 17; Gaps 6;

QY 7 FOQKHI-----INTPIICNTIMDNIIYVGGQCKRVNTFIISATTVAICTGV-INNM 59
DB 8 FORQMDPSSSSSNPNYCNLMRSR-NMTQGRCKPVPNTFVHESLADVOAVCSQINVK 66
QY 60 VLSTTRFOLNT-----CTRTSITPRP-CPYSSRTETNYICVKCE-NOY-PVHVF 104
DB 67 NGQTCYQSNSTMTHTDCRETGSSKYPNCAYKTSQOKYITVACEGHPVPVPHFD 120

RESULT 11
RNP_IGUIG
ID RNP_IGUIG STANDARD; PRT; 119 AA.
AC P80287;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).
OS Iguana iguana (Common iguana).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Iguania; Iguanidae; Iguaninae; Iguana.
OX NCBI_TaxID=8517;
RN [1]
RP SEQUENCE.
RX MEDLINE=94139745; PubMed=8307028;
RA Zhao W., Beintema J.J., Hofsteenge J.;
RT "The amino acid sequence of iguana (Iguana iguana) pancreatic ribonuclease.";
RL Eur. J. Biochem. 219:641-646 (1994).
RN [2]
RP REVISION TO 2.
CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-phosphates and 3'-phosphooligonucleotides ending in C-P or U-P with 2',3'-cyclic phosphate intermediates.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Pancreas.
CC -1- SIMILARITY: Belongs to the pancreatic ribonuclease family.
DR PIR: S41111; S41111.
DR HSP; P00656; 1LSQ.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; RNaseA; 1.
DR PRINTS: PR00794; RIBONUCLEASE.
DR ProDom: PD000535; RNaseA; 1.
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DR SMART; SM00092; RNase_Pc; 1.
 KW PROSITE; PS00127; RNase_PANCREATIC; 1.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT DISULFID 25 80 BY SIMILARITY.
 FT DISULFID 39 91 BY SIMILARITY.
 FT DISULFID 57 106 BY SIMILARITY.
 FT ACT_SITE 10 10 BY SIMILARITY.
 FT ACT_SITE 40 40 BY SIMILARITY.
 FT ACT_SITE 113 113 BY SIMILARITY.
 SQ SEQUENCE 119 AA; 13324 MW; 6072F85B7B15BD5A CRC64;
 Query Match 21.7%; Score 131.5; DB 1; Length 119;
 Best Local Similarity 30.4%; Pred. No. 2e-07;
 Matches 35; Conservative 16; Mismatches 51; Indels 13; Gaps 4;
 QY 2 QNATFOOKHI-----INTPLICNTIMDNNIYVGGCKRVNTFISSATTVKAIC-- 52
 DB 1 QOMSSFQNHDIYPTASNPAYCDLMQRR-NUNPTKCKTRNTFVHASPEIQOVCS 59
 QY 53 --TGVINNVLSSTTRFQNTCTRTSIT-PRPCPYSSRTETNYICVKENQYVPHF 104
 DB 60 GGTHYEDNLYDSNESFDLTDCKNVGCTAPSSCKYNGTPTCKEIRACENNQVPHF 114
 RESULT 12
 ID RNBR CAPCA STANDARD; PRT; 151 AA.
 AC P79351;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DE Ribonuclease, brain (EC 3.1.27.-) (BRB).
 OS Capreolus capreolus (Roe deer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervidae;
 OC Cervidae; Odocoileinae; Capreolus.
 OC NCBI_TaxID=9858;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98278842; PubMed=9611269;
 RA Bruckelman H.J., van der Munnik N., Kleineidam R.G., Furia A.,
 RA Beintema J.J.;
 RT "Secretory ribonuclease genes and pseudogenes in true ruminants.";
 RL Gene 212:259-268(1998).
 CC -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
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 CC or send an email to license@ebi-sib.ch).
 CC
 CC EMBL; Y11673; CAA72371.1; -.
 DR HSSP; P00656; 1SRN.
 DR InterPro; IPR001427; RNaseA.
 DR Pfam; PF00074; rnaseA; 1.
 DR PRINTS; PR00794; RIBONUCLEASE.
 DR ProDom; PD000535; RNaseA; 1.
 DR SMART; SM00092; RNase_Pc; 1.
 DR PROSITE; PS00127; RNase_PANCREATIC; 1.
 KW Hydrolyase; Nuclease; Endonuclease; Glycoprotein.
 FT ACT_SITE 41 41 BY SIMILARITY.
 FT DISULFID 26 84 BY SIMILARITY.
 FT DISULFID 40 95 BY SIMILARITY.
 FT DISULFID 58 110 BY SIMILARITY.
 FT DISULFID 65 72 BY SIMILARITY.
 FT CARBOHYD 62 62 N-LINKED (GLCNAC... (BY SIMILARITY).
 FT CARBOHYD 129 129 O-LINKED (BY SIMILARITY).
 FT CARBOHYD 133 133 O-LINKED (BY SIMILARITY).
 SQ SEQUENCE 123 AA; 14522 MW; B703B9839919FD2F CRC64;
 Query Match 21.0%; Score 127.5; DB 1; Length 123;
 Best Local Similarity 30.6%; Pred. No. 5.5e-07;
 Matches 33; Conservative 19; Mismatches 43; Indels 13; Gaps 5;
 QY 7 FQOKHIINTPI-----ICNTIMDNNIYVGGCKRVNTFISSATTVKAIC--TGVINNM 58
 DB 8 FLKHYDPSGTGHHDRVCNTMERR--NMTRPCKDNTTFIHGNSDDIRAVCDNRNGEYR 65
 QY 59 NVLSTTR--FQNTCTRTSITPR-PCPYSSRTETNYICVKENQYVPHF 103
 SQ SEQUENCE 151 AA; 16971 MW; 392D0B6302F006A6 CRC64;
 Query Match 21.2%; Score 128.5; DB 1; Length 151;
 Best Local Similarity 29.4%; Pred. No. 5.4e-07;
 Matches 35; Conservative 17; Mismatches 44; Indels 23; Gaps 6;
 QY 5 ATFOOKHI-----INTPLICNTIMDNNIYVGGCKRVNTFISSATTVKAICTGVINM 58
 DB 6 AKFRQHMDSGSSSSGNPNYCNQMKRR-RWTHGCKPNTFVHESLDNVKAVCS---QK 61
 QY 59 NVL-----STTRFQNTCTRTSITPR-PCPYSSRTETNYICVKENQ--YVPHF 104
 DB 62 NITCKNGQPCYNQSNSTNMTIDCRGTSSKYPNCAYKTSOKOKYITVACEGDPYVPHF 120
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 ID ANG2 BOVIN STANDARD; PRT; 123 AA.
 AC P80929;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DE Angiogenin-2 (EC 3.1.27.-).
 DE Angiogenin-2 (EC 3.1.27.-).
 GN ANG2.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
 OC Bovidae; Bovinae; Bos.
 OC NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE.
 RX TISSUE=Milk, and Serum;
 RX MEDLINE=97409980; PubMed=9266695;
 RA Straydom D.J., Bond M.D., Vallee B.L.;
 RT "An angiogenic protein from bovine serum and milk -- purification and
 RT primary structure of angiogenin-2.";
 RL Eur. J. Biochem. 247:535-544(1997).
 CC -!- FUNCTION: BINDS TIGHTLY TO PLACENTAL RIBONUCLEASE INHIBITOR AND
 CC HAS VERY LOW RIBONUCLEASE ACTIVITY. HAS POTENT ANGIOGENIC
 CC ACTIVITY. ANGIOGENIN INDUCES VASCULARIZATION OF NORMAL AND
 CC MALIGNANT TISSUES. ABOLISHES PROTEIN SYNTHESIS BY SPECIFICALLY
 CC HYDROLYZING CELLULAR RNAs.
 CC -!- TISSUE SPECIFICITY: SERUM, AND MILK.
 CC -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
 DR HSSP; P10152; 1AGI.
 DR InterPro; IPR001427; RNaseA.
 DR Pfam; PF00074; rnaseA; 1.
 DR PRINTS; PR00794; RIBONUCLEASE.
 DR ProDom; PD000535; RNaseA; 1.
 DR SMART; SM00092; RNase_Pc; 1.
 DR PROSITE; PS00127; RNase_PANCREATIC; 1.
 KW Hydrolyase; Nuclease; Endonuclease; Angiogenesis;
 KW Protein synthesis inhibitor; Glycoprotein;
 KW Pyrolidone carboxylic acid.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT ACT_SITE 12 12 BY SIMILARITY.
 FT ACT_SITE 39 39 BY SIMILARITY.
 FT ACT_SITE 113 113 BY SIMILARITY.
 FT DISULFID 25 80
 FT DISULFID 38 91
 FT DISULFID 56 106
 FT CARBOHYD 33 33 N-LINKED (GLCNAC...).
 SQ SEQUENCE 123 AA; 14522 MW; B703B9839919FD2F CRC64;
 Query Match 21.0%; Score 127.5; DB 1; Length 123;
 Best Local Similarity 30.6%; Pred. No. 5.5e-07;
 Matches 33; Conservative 19; Mismatches 43; Indels 13; Gaps 5;
 QY 7 FQOKHIINTPI-----ICNTIMDNNIYVGGCKRVNTFISSATTVKAIC--TGVINNM 58
 DB 8 FLKHYDPSGTGHHDRVCNTMERR--NMTRPCKDNTTFIHGNSDDIRAVCDNRNGEYR 65
 QY 59 NVLSTTR--FQNTCTRTSITPR-PCPYSSRTETNYICVKENQYVPHF 103

[illegible]

Db 122 G 122

Search completed: January 22, 2004, 12:02:09
Job time : 6.65169 secs

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OM protein - protein search, using sw model

Run on: January 22, 2004, 12:02:15 ; Search time 26.3989 Seconds
(without alignments)
869.271 Million cell updates/sec

Title: US-09-622-613C-17

Perfect score: 607

Sequence: 1 MQNWATFQKHINTPIICN.....ICVKCNQYVHFAGIGRCP 111

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 777136 seqs, 206736638 residues

Total number of hits satisfying chosen parameters: 777136

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Databases :

- Published Applications AA:*
- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
 - 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
 - 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
 - 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
 - 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
 - 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
 - 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
 - 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
 - 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
 - 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
 - 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
 - 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
 - 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
 - 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
 - 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
 - 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
 - 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
 - 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	607	100.0	111	11	US-09-961-400-17	Sequence 17, Appl
2	602	99.2	110	11	US-09-948-391A-15	Sequence 15, Appl
3	602	99.2	110	11	US-09-961-400-15	Sequence 15, Appl
4	602	99.2	111	11	US-09-948-391A-26	Sequence 26, Appl
5	602	99.2	111	11	US-09-961-400-26	Sequence 26, Appl
6	601	99.0	111	11	US-09-948-391A-17	Sequence 17, Appl
7	601	99.0	111	11	US-09-948-391A-21	Sequence 21, Appl
8	601	99.0	111	11	US-09-961-400-21	Sequence 21, Appl
9	601	99.0	117	11	US-09-948-391A-22	Sequence 22, Appl
10	601	99.0	117	11	US-09-961-400-22	Sequence 22, Appl
11	597	98.4	110	11	US-09-948-391A-24	Sequence 24, Appl
12	597	98.4	110	11	US-09-961-400-24	Sequence 24, Appl
13	596	98.2	110	11	US-09-961-400-19	Sequence 19, Appl
14	590	97.2	110	11	US-09-948-391A-19	Sequence 19, Appl
15	286.5	47.2	105	11	US-09-948-391A-6	Sequence 6, Appl

16	286.5	47.2	105	11	US-09-961-400-6	Sequence 6, Appl
17	283.5	46.7	111	11	US-09-961-400-9	Sequence 9, Appl
18	282.5	46.5	105	15	US-10-153-882-2	Sequence 2, Appl
19	281.5	46.4	104	11	US-09-961-400-2	Sequence 2, Appl
20	281.5	46.4	105	11	US-09-948-391A-13	Sequence 13, Appl
21	281.5	46.4	105	11	US-09-961-400-13	Sequence 13, Appl
22	281.5	46.4	127	11	US-09-948-391A-28	Sequence 28, Appl
23	281.5	46.4	127	11	US-09-961-400-28	Sequence 28, Appl
24	280.5	46.2	104	11	US-09-948-391A-2	Sequence 2, Appl
25	280.5	46.2	105	11	US-09-961-400-8	Sequence 8, Appl
26	276.5	45.6	104	11	US-09-948-391A-11	Sequence 11, Appl
27	276.5	45.6	104	11	US-09-961-400-11	Sequence 11, Appl
28	275.5	45.4	104	11	US-09-948-391A-4	Sequence 4, Appl
29	275.5	45.4	104	11	US-09-961-400-4	Sequence 4, Appl
30	272.5	44.9	104	10	US-09-986-119-1	Sequence 1, Appl
31	272.5	44.9	104	11	US-09-918-887-1	Sequence 1, Appl
32	271.5	44.7	105	11	US-09-948-391A-8	Sequence 8, Appl
33	271.5	44.7	111	11	US-09-948-391A-9	Sequence 9, Appl
34	206	33.9	83	10	US-09-986-119-3	Sequence 3, Appl
35	206	33.9	83	11	US-09-918-887-3	Sequence 3, Appl
36	163	26.9	169	13	US-10-016-447-2	Sequence 2, Appl
37	131.5	21.7	119	12	US-10-074-978A-139	Sequence 139, App
38	121	19.9	99	12	US-10-074-978A-141	Sequence 141, App
39	117	19.3	147	10	US-09-731-872-254	Sequence 254, App
40	117	19.3	147	12	US-09-876-997-254	Sequence 254, App
41	114.5	18.9	124	10	US-09-981-286A-8	Sequence 8, Appl
42	114	18.8	124	13	US-10-016-447-5	Sequence 5, Appl
43	113	18.6	131	13	US-10-016-447-6	Sequence 6, Appl
44	113	18.6	147	9	US-09-286-240-6	Sequence 6, Appl
45	113	18.6	147	9	US-09-863-777-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1

US-09-961-400-17
; Sequence 17, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: GOLDENBERG, DAVID M.
; APPLICANT: NEWTON, DIANNE L.
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 018733/1059
; CURRENT APPLICATION NUMBER: US/09/961,400
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 09/622,613
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/079,751
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Rana catesbeiana
US-09-961-400-17

Query Match	100.0%	Score	607	DB	11	Length	111
Best Local Similarity	100.0%	Pred. No.	1.8e-61				
Matches	111	Conservative	0	Mismatches	0	Indels	0
Gaps	0						
Qy	1	MQNWATFQKHINTPIICNTIMDNNIYVGGCKRVNTFIISATTVKATCTGVINNV	60				
Db	1	MQNWATFQKHINTPIICNTIMDNNIYVGGCKRVNTFIISATTVKATCTGVINNV	60				
Qy	61	LSTTRFQNTCTRTSTTPRCPYSSRTETNYICVKCNQYVHFAGIGRCP	111				
Db	61	LSTTRFQNTCTRTSTTPRCPYSSRTETNYICVKCNQYVHFAGIGRCP	111				

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RESULT 2
US-09-948-391A-15
; Sequence 15, Application US/09948391A
; Publication No. US20030027311A1
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: The United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Recombinant Anti-Tumor RNase
; FILE REFERENCE: 015280-343110US
; CURRENT APPLICATION NUMBER: US/09/948,391A
; PRIOR FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 60/079,751
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/622,613
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Rana
; OTHER INFORMATION: catesbeiana oocyte ribonuclease (RaCOR1) synthetic
; OTHER INFORMATION: gene modified to use E. coli preferred codons
US-09-948-391A-15

Query Match          99.2%; Score 602; DB 11; Length 110;
Best Local Similarity 100.0%; Pred. No. 6.6e-61;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  2 QNWATFOQKHIIINTPIICNTIMDNNIYIVGGQCKRVNTFISSATTVKAICTGVINMNV 61
Db  1 QNWATFOQKHIIINTPIICNTIMDNNIYIVGGQCKRVNTFISSATTVKAICTGVINMNV 60

Qy  62 STTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
Db  61 STTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110

RESULT 3
US-09-961-400-15
; Sequence 15, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: GOLDENBERG, DAVID M.
; APPLICANT: NEWTON, DIANNE L.
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 018733/1059
; CURRENT APPLICATION NUMBER: US/09/961,400
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 09/622,613
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/079,751
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Rana catesbeiana
US-09-961-400-15
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Query Match          99.2%; Score 602; DB 11; Length 110;
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Qy  62 STTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
Db  61 STTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110

RESULT 4
US-09-948-391A-26
; Sequence 26, Application US/09948391A
; Publication No. US20030027311A1
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: The United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Recombinant Anti-Tumor RNase
; FILE REFERENCE: 015280-343110US
; CURRENT APPLICATION NUMBER: US/09/948,391A
; PRIOR FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 60/079,751
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/622,613
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Rana
; OTHER INFORMATION: catesbeiana ribonuclease with Met at position 1
; OTHER INFORMATION: and Gln2Ser substitution (Met(-1) RaCOR1 Q1S)
US-09-948-391A-26

Query Match          99.2%; Score 602; DB 11; Length 111;
Best Local Similarity 99.1%; Pred. No. 6.6e-61;
Matches 110; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db  1 MSNWATFOQKHIIINTPIICNTIMDNNIYIVGGQCKRVNTFISSATTVKAICTGVINMNV 60

Qy  61 LSTTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
Db  61 LSTTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111

RESULT 5
US-09-961-400-26
; Sequence 26, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: GOLDENBERG, DAVID M.
; APPLICANT: NEWTON, DIANNE L.
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 018733/1059
; CURRENT APPLICATION NUMBER: US/09/961,400
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 09/622,613
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Matches 109; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
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DB 61 LSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111

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US-09-948-391A-22
; Sequence 22, Application US/09948391A
; Publication No. US20030027311A1
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: The United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Recombinant Anti-Tumor RNase
; FILE REFERENCE: 015280-343110US
; CURRENT APPLICATION NUMBER: US/09/948,391A
; CURRENT FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 60/079,751
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/622,613
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Rana
; OTHER INFORMATION: catesbeiana ribonuclease with (His)6 tag, Met at
; OTHER INFORMATION: position 7, Met23Leu and Met58Leu substitutions
; OTHER INFORMATION: (recombinant Met(-1) RacOR1 Met22Leu Met57Leu-(His)6)
US-09-948-391A-22

Query Match 99.0%; Score 601; DB 11; Length 117;
Best Local Similarity 98.2%; Pred. No. 9.2e-61;
Matches 109; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 MONWATFOOKHIIINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINNV 60
DB 7 MONWATFOOKHIIINTPIICNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVINLV 66
QY 61 LSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
DB 67 LSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 117

RESULT 10
US-09-961-400-22
; Sequence 22, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: GOLDENBERG, DAVID M.
; APPLICANT: NEWTON, DIANNE L.
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
; FILE REFERENCE: 018733/1059
; CURRENT APPLICATION NUMBER: US/09/961,400
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 09/622,613
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US99/06641
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; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/079,751
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Rana catesbeiana
US-09-961-400-22

Query Match 99.0%; Score 601; DB 11; Length 117;
Best Local Similarity 98.2%; Pred. No. 9.2e-61;
Matches 109; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 MONWATFOOKHIIINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINNV 60
DB 7 MONWATFOOKHIIINTPIICNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVINLV 66
QY 61 LSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
DB 67 LSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 117

RESULT 11
US-09-948-391A-24
; Sequence 24, Application US/09948391A
; Publication No. US20030027311A1
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: The United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Recombinant Anti-Tumor RNase
; FILE REFERENCE: 015280-343110US
; CURRENT APPLICATION NUMBER: US/09/948,391A
; CURRENT FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 60/079,751
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/622,613
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 24
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Rana
; OTHER INFORMATION: catesbeiana ribonuclease with Gln1Ser substitution
; OTHER INFORMATION: (recombinant RacOR1 Q1S)
US-09-948-391A-24

Query Match 98.4%; Score 597; DB 11; Length 110;
Best Local Similarity 100.0%; Pred. No. 2.4e-60;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 NWATFOOKHIIINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINNVLS 62
DB 2 NWATFOOKHIIINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINNVLS 61
QY 63 TTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
DB 62 TTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110

RESULT 12
US-09-961-400-24
; Sequence 24, Application US/09961400
; Publication No. US20030124131A1
```

GENERAL INFORMATION:
APPLICANT: RYBAK, SUSANNA M.
APPLICANT: GOLDENBERG, DAVID M.
APPLICANT: NEWTON, DIANNE L.
TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
FILE REFERENCE: 018733/1059
CURRENT APPLICATION NUMBER: US/09/961,400
CURRENT FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: 09/622,613
PRIOR FILING DATE: 2000-08-17
PRIOR APPLICATION NUMBER: PCT/US99/06641
PRIOR FILING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: 60/079,751
PRIOR FILING DATE: 1998-03-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 24
LENGTH: 110
TYPE: PRT
ORGANISM: Rana catesbeiana
US-09-961-400-24

Query Match 98.4%; Score 597; DB 11; Length 110;
Best Local Similarity 100.0%; Pred. No. 2.4e-60;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 NWATFOOKHIINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINMNVLS 62
Db 2 NWATFOOKHIINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINMNVLS 61

Qy 63 TTRFQNLCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
Db 62 TTRFQNLCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110

RESULT 13
US-09-961-400-19
Sequence 19, Application US/09961400
Publication No. US20030124131A1
GENERAL INFORMATION:
APPLICANT: RYBAK, SUSANNA M.
APPLICANT: GOLDENBERG, DAVID M.
APPLICANT: NEWTON, DIANNE L.
TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
FILE REFERENCE: 018733/1059
CURRENT APPLICATION NUMBER: US/09/961,400
CURRENT FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: 09/622,613
PRIOR FILING DATE: 2000-08-17
PRIOR APPLICATION NUMBER: PCT/US99/06641
PRIOR FILING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: 60/079,751
PRIOR FILING DATE: 1998-03-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 19
LENGTH: 110
TYPE: PRT
ORGANISM: Rana catesbeiana
US-09-961-400-19

Query Match 98.2%; Score 596; DB 11; Length 110;
Best Local Similarity 98.2%; Pred. No. 3.2e-60;
Matches 108; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QNWATFOOKHIINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINMNVL 61
Db 1 QNWATFOOKHIINTPIICNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVINLNL 60

Qy 62 STTRFQNLCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
Db 61 STTRFQNLCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110

Db 61 STTRFQNLCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110

RESULT 14
US-09-948-391A-19
Sequence 19, Application US/09948391A
Publication No. US20030027311A1
GENERAL INFORMATION:
APPLICANT: RYBAK, SUSANNA M.
APPLICANT: NEWTON, DIANNE L.
APPLICANT: The United States of America
APPLICANT: as represented by The Secretary of the
TITLE OF INVENTION: Department of Health and Human Services
TITLE OF INVENTION: Recombinant Anti-Tumor RNase
FILE REFERENCE: 015280-343110US
CURRENT APPLICATION NUMBER: US/09/948,391A
CURRENT FILING DATE: 2002-05-10
PRIOR APPLICATION NUMBER: US 60/079,751
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: WO PCT/US99/06641
PRIOR FILING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: US 09/622,613
PRIOR FILING DATE: 2000-08-17
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 19
LENGTH: 110
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Rana
OTHER INFORMATION: catesbeiana ribonuclease with Met22Leu and
OTHER INFORMATION: Met57Leu substitutions (recombinant RacORI
OTHER INFORMATION: Met22Leu Met57Leu)
US-09-948-391A-19

Query Match 97.2%; Score 590; DB 11; Length 110;
Best Local Similarity 97.3%; Pred. No. 1.5e-59;
Matches 107; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QNWATFOOKHIINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINMNVL 61
Db 1 QNWATFOOKHIINTPIICNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVINLNL 60

Qy 62 STTRFQNLCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
Db 61 STTRFQNLCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110

RESULT 15
US-09-948-391A-6
Sequence 6, Application US/09948391A
Publication No. US20030027311A1
GENERAL INFORMATION:
APPLICANT: RYBAK, SUSANNA M.
APPLICANT: NEWTON, DIANNE L.
APPLICANT: The United States of America
APPLICANT: as represented by The Secretary of the
TITLE OF INVENTION: Department of Health and Human Services
TITLE OF INVENTION: Recombinant Anti-Tumor RNase
FILE REFERENCE: 015280-343110US
CURRENT APPLICATION NUMBER: US/09/948,391A
CURRENT FILING DATE: 2002-05-10
PRIOR APPLICATION NUMBER: US 60/079,751
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: WO PCT/US99/06641
PRIOR FILING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: US 09/622,613
PRIOR FILING DATE: 2000-08-17
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6
LENGTH: 105


```
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Rana pipiens
; OTHER INFORMATION: ribonuclease with Met at position 1 (recombinant)
; OTHER INFORMATION: Met (-1) RnPLR1)
US-09-948-391A-6

Query Match      47.2%; Score 286.5; DB 11; Length 105;
Best Local Similarity 50.0%; Pred.No. 5.4e-25;
Matches 56; Conservative 15; Mismatches 32; Indels 9; Gaps 4;

Qy    1 MQNWTFFQQKHINT-PIICNTMDNNIYIVGGCKRVNTFIASSATTVKAICTGVI-NM 58
      |||||:||||:::||||:::||||:::||||:::||||:::||||:::||||::
Db     1 MQDWLIFQKGLHINTRDVDCCNIIMSTNLF----HKDKQNTFYISRPPEPKAI CKGIASK 56

Qy    59 NVLSSTRFQLNCTTTSITPRCPYSRSRTETNYICVKCENQYPVHFAGIGRC 110
      ||||:::||||:::||||:::||||:::||||:::||||:::||||:::||||::
Db     57 NVLTTSEFYLSDC---NVTSRPCPKYLKKKSNTFPVCVTCENQOAPVHFVGVGHC 105
```

Search completed: January 22, 2004, 12:12:26
Job time : 27.3989 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 22, 2004, 12:01:20 ; Search time 12.4719 Seconds
(without alignment)
855.901 Million cell updates/sec

Title: US-09-622-613C-17

Perfect score: 607

Sequence: 1 MQNWATFOQKHINTPIICN.....ICVKCENQYPVHPAGIGRCP 111

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_76.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	588.5	97.0	111	2 A27121	ribonuclease-relat
2	455	75.0	111	1 JX0120	ribonuclease-relat
3	374	61.6	111	2 JX0085	pancreatic ribonuc
4	274.5	45.2	104	2 A39035	ribonuclease-relat
5	135.5	22.3	124	1 NRWHK	pancreatic ribonuc
6	135.5	22.3	145	1 A35932	angiogenin precurs
7	133.5	22.0	167	2 S20066	pancreatic-type ri
8	132.5	21.8	124	1 NRP6	pancreatic ribonuc
9	131.5	21.7	119	2 S41111	pancreatic ribonuc
10	122.5	20.2	124	1 NRPH	pancreatic ribonuc
11	122	20.1	122	1 NRKGR	pancreatic ribonuc
12	120.5	19.9	128	1 NRCU	pancreatic ribonuc
13	120.5	19.9	149	1 NRMS	pancreatic ribonuc
14	119.5	19.7	123	1 A43825	pancreatic ribonuc
15	118.5	19.5	128	1 NRGPB	angiogenin - pig
16	117.5	19.4	128	1 NRHO	pancreatic ribonuc
17	116.5	19.2	124	1 NRCM	pancreatic ribonuc
18	116.5	19.2	124	1 NRCMM	pancreatic ribonuc
19	116.5	19.2	124	1 NRCMB	pancreatic ribonuc
20	116.5	19.2	128	1 NRKS	pancreatic ribonuc
21	114.5	18.9	124	2 S08549	ribonuclease - dom
22	114	18.8	125	1 A32474	angiogenin [valida
23	113.5	18.7	124	1 NRDEN	angiogenin precurs
24	113	18.6	127	1 NRHUG	pancreatic ribonuc
25	112.5	18.5	124	1 NRGF	pancreatic ribonuc
26	112.5	18.5	124	1 NRDEO	pancreatic ribonuc
27	112	18.5	125	1 B43825	angiogenin - rabbi
28	111.5	18.4	130	2 S22808	pancreatic ribonuc
29	110.5	18.2	124	1 NRBOB	pancreatic ribonuc

30	110.5	18.2	124	1 NRWB	pancreatic ribonuc
31	110.5	18.2	124	1 NREKN	pancreatic ribonuc
32	110.5	18.2	124	2 S07141	pancreatic ribonuc
33	110.5	18.2	150	1 NRBO	pancreatic ribonuc
34	110.5	18.2	158	2 I61900	eosinophil-derived
35	109.5	18.0	124	1 NRSH	pancreatic ribonuc
36	108.5	17.9	119	2 JX0115	pancreatic ribonuc
37	108.5	17.9	124	1 NRCB	pancreatic ribonuc
38	108.5	17.9	152	1 NRRT	pancreatic ribonuc
39	106.5	17.5	124	1 NRHP	pancreatic ribonuc
40	106.5	17.5	125	4 A47498	seminal ribonuclea
41	106.5	17.5	150	1 NRBO	ribonuclea
42	104.5	17.2	124	1 NRGN	pancreatic ribonuc
43	104.5	17.2	124	1 NRDEF	pancreatic ribonuc
44	104	17.1	125	2 S04503	pancreatic ribonuc
45	103.5	17.1	124	2 S08546	pancreatic ribonuc

ALIGNMENTS

RESULT 1

A27121 ribonuclease-related sialic acid-binding lectin - bullfrog

C:Species: Rana catesbeiana (bullfrog)

C:Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 30-Jun-1993
C:Accession: A27121

R:Titani, K.; Takio, K.; Kuwada, M.; Nitta, K.; Sakakibara, F.; Kawachi, H.; Takayanagi,

Biochemistry 26, 2189-2194, 1987

A:Title: Amino acid sequence of sialic acid-binding lectin from frog (Rana catesbeiana)

A:Reference number: A27121; MUID:87299649; PMID:3304421

A:Accession: A27121

A:Molecule type: protein

A:Residues: 1-111 <111>

C:Superfamily: pancreatic ribonuclease

C:Keywords: lectin

Query Match 97.0%; Score 588.5; DB 2; Length 111;

Best Local Similarity 98.2%; Pred. No. 1.4e-51;

Matches 109; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

Qy	2	QNWATFOQKHINTPII-CNTIMDNIIYVGQCKRVNTFIISATTVKAICTGVNNV 60
Db	1	ENWATFOQKHINTPIINCNTIMDNIIYVGQCKRVNTFIISATTVKAICTGVNNV 60
Qy	61	LSTTRFQNLCTRTSITPRCPYSSRTETNYICVKCENQYPVHPAGIGRCP 111
Db	61	LSTTRFQNLCTRTSITPRCPYSSRTETNYICVKCENQYPVHPAGIGRCP 111

RESULT 2

JX0120 ribonuclease-related sialic acid-binding lectin - Japanese frog

C:Species: Rana japonica (Japanese frog)

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: JX0120

R:Kamiya, Y.; Oyama, F.; Oyama, R.; Sakakibara, F.; Nitta, K.; Kawachi, H.; Takayanagi,

J. Biochem. 108, 139-143, 1990

A:Title: Amino acid sequence of a lectin from Japanese frog (Rana japonica) eggs.

A:Reference number: JX0120; MUID:91035319; PMID:2229005

A:Accession: JX0120

A:Molecule type: protein

A:Residues: 1-111 <KAM>

A:Experimental source: egg

C:Superfamily: pancreatic ribonuclease

C:Keywords: lectin; pyroglyutamic acid

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F:19-72,34-82,52-97,94-111/Disulfide bonds: #status experimental

Query Match

Best Local Similarity 75.0%; Score 455; DB 1; Length 111;

Matches 87; Conservative 7; Mismatches 15; Indels 2; Gaps 2;

```
OY 2 QNWATFOQKHINTP-IICNTIMDNIIYVGGCKRVNTFISSATTVAICTGV-INNN 59
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 QNWAQFQKHINTPINSINCNTIMDSKIIYVGGCKRVNTFISSATTVAICSGASTRN 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

OY 60 VLSTTRFQNTCTRTSITPRCPYSSRTETNYICVKCENQYVHPFAGIGRC 110
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 VLSTTRFQNTCTRTSITPRCPYSSRTETNYICVKCENRQVHPFAGIGRC 111
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 3
JX0085
pancreatic ribonuclease (EC 3.1.27.5) - bullfrog
C:Species: Rana catesbeiana (bullfrog)
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 05-Aug-1994
C:Accession: JX0085
R:Nitta, K.; Katayama, N.; Okabe, Y.; Iwama, M.; Watanabe, H.; Abe, Y.; Okazaki, T.; Ohguchi, T.;
J. Biochem. 106, 729-735, 1989
A:Title: Primary structure of a ribonuclease from bullfrog (Rana catesbeiana) liver.
A:Reference number: JX0085; MUID:90130374; PMID:2613682
A:Accession: JX0085
A:Molecule type: protein
A:Residues: 1-111 <NT>
C:Superfamily: pancreatic ribonuclease
C:Keywords: hydrolase; pyroglyutamic acid
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:10.35.104/Active site: His, Lys, His #status predicted
F:19-72,34-82,52-97,94-111/Disulfide bonds: #status predicted

Query Match 61.6%; Score 374; DB 2; Length 111;
Best Local Similarity 65.8%; Pred. No. 2.9e-30;
Matches 73; Conservative 9; Mismatches 27; Indels 2; Gaps 2;

OY 2 QNWATFOQKHINTPII-CNTIMDNIIYVGGCKRVNTFISSATTVAICTGVI-NNN 59
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 QNWAQFQKHIRSTSIDCNTIMDKAIIYVGGCKRVNTFISSADNVKAICSGVSPDRK 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

OY 60 VLSTTRFQNTCTRTSITPRCPYSSRTETNYICVKCENQYVHPFAGIGRC 110
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 ELSTTSFKLNTCIRDSITPRCPYHSPDNKKICVKCEKQLPVPFVGKIC 111
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 4
A39035
ribonuclease-related anti-tumor protein - northern leopard frog (fragment)
C:Species: Rana pipiens (northern leopard frog)
C:Date: 31-Jul-1991 #sequence_revision 31-Jul-1991 #text_change 30-Jun-1993
C:Accession: A39035
R:Ardelet, W.; Mikulski, S.M.; Shogen, K.
J. Biol. Chem. 266, 245-251, 1991
A:Title: Amino acid sequence of an anti-tumor protein from Rana pipiens oocytes and earl
A:Reference number: A39035; MUID:91093131; PMID:1985896
A:Accession: A39035
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-104 <ARD>
C:Superfamily: pancreatic ribonuclease

Query Match 45.2%; Score 274.5; DB 2; Length 104;
Best Local Similarity 48.6%; Pred. No. 2.1e-20;
Matches 54; Conservative 16; Mismatches 32; Indels 9; Gaps 4;

OY 2 QNWATFOQKHINT-PIICNTIMDNIIYVGGCKRVNTFISSATTVAICTGVI-NNN 59
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 EDWLTFQKHINTTRDVEDCDNIMSTNLF----HCKDKNTFIYSRPEPVKAICGIIASKN 56
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

OY 60 VLSTTRFQNTCTRTSITPRCPYSSRTETNYICVKCENQYVHPFAGIGRC 110
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 57 VLTTFSEFYLSDC---NVTSRPCKYKKSSTNKFVCVTCBNQAPVHPFVGSGC 104
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 5
NRWHK
pancreatic ribonuclease (EC 3.1.27.5) - minke whale
```

```
N:Alternate names: RNase 1; RNase A
C:Species: Balaenoptera acutorostrata (minke whale, lesser rorqual)
C:Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 03-Jun-1994
C:Accession: A00818
R:Emmens, M.; Welling, G.W.; Beintema, J.J.
Biochem. J. 157, 317-323, 1976
A:Title: The amino acid sequence of pike whale (lesser rorqual) pancreatic ribonuclease.
A:Reference number: A00818; MUID:76277855; PMID:962870
A:Accession: A00818
A:Molecule type: protein
A:Residues: 1-124 <EMM>
C:Superfamily: pancreatic ribonuclease
C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F:12.41.119/Active site: His, Lys, His #status predicted
F:26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted
F:76/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental

Query Match 22.3%; Score 135.5; DB 1; Length 124;
Best Local Similarity 33.3%; Pred. No. 1.7e-06;
Matches 39; Conservative 16; Mismatches 39; Indels 23; Gaps 7;

OY 7 FQKXHI-----NTPICNTIMDNIIYVGGCKRVNTFISSATTVAICTGVINNV 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 8 FQKHMDSGNSPGNNPNYCNQMMRR-RDTQGRCKPVNTFVHESLEDVKAVCS---QKNV 63
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

OY 61 L-----STTRFQNTCTRTSITPRP-CPYSSRTETNYICVKE-NOY-PVHF 104
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 64 LCKNGRTNVCYESNTMHTDCRQTGSSKYPNCAYKTSOKERHIIIVACENPVVPVHF 120
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 6
A35932
angiogenin precursor - mouse
N:Alternate names: angiogenesis factor
N:Contains: ribonuclease (EC 3.1.27.-)
C:Species: Mus musculus (house mouse)
C:Date: 09-Nov-1990 #sequence_revision 09-Nov-1990 #text_change 18-Jun-1999
C:Accession: A35932
R:Bond, M.D.; Vallee, B.L.
Biochem. Biophys. Res. Commun. 171, 988-995, 1990
A:Title: Isolation and sequencing of mouse angiogenin DNA.
A:Reference number: A35932; MUID:91025023; PMID:222458
A:Accession: A35932
A>Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-145 <BN>
A:Cross-references: GB:U22516; NID:9726325; PIDN:AAA91366.1; PID:g726326
C:Genetics:
A:Introns: #status absent
C:Function:
A:Description: hydrolyzes tRNA; induces vascularization of normal and malignant tissues
C:Superfamily: pancreatic ribonuclease
C:Keywords: angiogenesis; hydrolase; nucleic acid degradation; pyroglyutamic acid
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-145/Product: angiogenin #status predicted <MAT>
F:25/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
F:37.64.137/Active site: His, Lys, His #status predicted
F:50-104,63-115,81-130/Disulfide bonds: #status predicted

Query Match 22.3%; Score 135.5; DB 1; Length 145;
Best Local Similarity 39.5%; Pred. No. 2e-06;
Matches 30; Conservative 12; Mismatches 29; Indels 5; Gaps 3;

OY 34 CKRVNTFISSATTVAIC---TGVINNV-LSTTRFQNTCTRTSITPR-PCPYSSRTE 88
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 63 CKDVTPIHGKSNIKAIKANGANGPYRENLRMSKSPQVTTCKHTGGSPRPPCQYRASG 122
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

OY 89 TNYICVKCENQYVHPF 104
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 123 FRHVVIACENGLPVHF 138
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 7
```

S20066
pancreatic-type ribonuclease (EC 3.1.27.5) BRB precursor, brain - bovine
C:Species: Bos primigenius taurus (cattle)
C>Date: 22-Nov-1993 #sequence_revision 12-May-1995 #text_change 22-Jun-1999
C:Accession: S20066; JX0056
R:Sasso, M.P.; Carsana, A.; Confalone, E.; Cosi, C.; Sorrentino, S.; Viola, M.; Palmieri,
Nucleic Acids Res. 19, 6469-6474, 1991
A>Title: Molecular cloning of the gene encoding the bovine brain ribonuclease and its ex
A:Reference number: S20066; MUID:92093604; PMID:1754384
A:Accession: S20066
A:Molecule type: DNA
A:Residues: 1-167 <SAS>
A:Cross-references: EMBL:X59767; NID:g150; PIDN:CAA42439.1; PID:g151
R:Watanabe, H.; Katoh, H.; Ishii, M.; Komoda, Y.; Sanda, A.; Takizawa, Y.; Ohgi, K.; Iri
J. Biochem. 104, 939-945, 1988
A>Title: Primary structure of a ribonuclease from bovine brain.
A:Reference number: JX0056; MUID:9214015; PMID:3243767
A:Accession: JX0056
A:Molecule type: protein
A:Residues: 27-154,'S',156-166 <WAT>
A:Experimental source: brain
C:Superfamily: pancreatic ribonuclease
C:Keywords: glycoprotein; hydrolase
F:38,67,145/Active site: His, Lys, His #status predicted
F:52-110,66-121,84-136,91-98/disulfide bonds: #status experimental
F:88/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:155/Binding site: carbohydrate (Thr) (covalent) #status experimental
F:159/Binding site: carbohydrate (Ser) (covalent) #status experimental

Query Match 22.0%; Score 133.5; DB 2; Length 167;
Best Local Similarity 31.4%; Pred. No. 3.6e-06;
Matches 38; Conservative 17; Mismatches 43; Indels 23; Gaps 7;

Qy 5 ATFOQKH-----INTPICTIMDNVIYVGCGKRVNTFISSATTVKAICTGVNM 58
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 32 AKFRQRHMGSGSSSNPNVCNQMKRR-RMTGRCRPVNIFVHESLDDVKAVCS---OK 87
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

Qy 59 NVL-----STTRFQLNCTRTSIITPRP-CPYSSRTETNYICVCKE-NQY-FVHFA 105
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 88 NITCKNGHPNCYQSKSTMSITDCRETGS SKVPNCAYKTSQKVITVACEGNFPVPVFD 147
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

Qy 106 G 106
|
Db 148 G 148

RESULT 8
NRPC
pancreatic ribonuclease (EC 3.1.27.5) - pig
N:Alternate names: RNase 1; RNase A
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 03-Jun-1994
C:Accession: A92071; A91391; A00816
R:Jackson, R.L.; Hirs, C.H.W.
J. Biol. Chem. 245, 637-653, 1970
A>Title: The primary structure of porcine pancreatic ribonuclease. II. The amino acid se
A:Reference number: A92071; MUID:70104197; PMID:5460946
A:Accession: A92071
A:Molecule type: protein
A:Residues: 1,'O',3-124 <JAC>
R:Wierenga, R.K.; Huizinga, J.D.; Gaasstra, W.; Wellings, G.W.; Beintema, J.J.
FEBS Lett. 31, 181-185, 1973
A>Title: Affinity chromatography of porcine pancreatic ribonuclease and reinvestigation
A:Reference number: A91391
A:Accession: A91391
A:Molecule type: protein
A:Residues: 1-124 <WIE>
R:Phelan, J.J.; Hirs, C.H.W.
J. Biol. Chem. 245, 654-661, 1970
A>Title: The primary structure of porcine pancreatic ribonuclease. III. The disulfide bo
A:Reference number: A92072; MUID:70104198; PMID:4904878
A:Contents: annotation; disulfide bonds
C:Superfamily: pancreatic ribonuclease

C;Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F;12,41,119/Active site: His, Lys, His #status predicted
F;21,34,76/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;26-84,40-95,58-110,65-72/Dsulfide bonds: #status experimental

Query Match 21.8%; Score 132.5; DB 1; Length 124;
Best Local Similarity 31.6%; Pred.No.3.3e-06;
Matches 36; Conservative 19; Mismatches 42; Indels 17; Gaps 6;

QY 7 FQKHII-----INTPIICNTIMNNIIVIGGCKRVNFTFISSATTVKAICTGV-INNN 59
| | | : | : | : | : | : | : | : | : | : | : | : | : |
Db 8 FORQHWDPDSSSNSSNYCNLWMSRR-NMTQGRCKPVNTFVHESLADVAQVCQSINVNCK 66
| | | : | : | : | : | : | : | : | : | : | : | : | : |

QY 60 VLSTRFQLNT-----CTRISITPRP-CPYSSRRTETNYICKENQ--YPVHF 104
| | | : | : | : | : | : | : | : | : | : | : | : | : |
Db 67 NGQTNCYOSNSTWHITDCROTGSSEKYPNCAYKASOEQHIIIVACEGNPPVPVHF 120
| | | : | : | : | : | : | : | : | : | : | : | : | : |

RESULT 9
S41111
pancreatic ribonuclease - common iguana
C;Species: Iguana iguana (common iguana)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 21-Aug-1998
C;Accession: S41111
R;Zhao, W.; Beintema, J.J.; Hofsteenge, J.
Eur. J. Biochem. 219, 641-646, 1994
A;Title: The amino acid sequence of iguana (Iguana iguana) pancreatic ribonuclease.
A;Reference number: S41111; MUID:94139745; PMID:8307028
A;Accession: S41111
A>Status: preliminary
A:Molecule type: protein
A;Residues: 1-119 <ZHA>
C;Superfamily: pancreatic ribonuclease

Query Match 21.7%; Score 131.5; DB 2; Length 119;
Best Local Similarity 30.4%; Pred.No.4e-06;
Matches 35; Conservative 16; Mismatches 51; Indels 13; Gaps 4;

QY 2 QNWATTFQOKHI-----INTPIICNTIMNNIIVIGGCKRVNFTFISSATTVKAIC-- 52
| | | : | : | : | : | : | : | : | : | : | : | : | : |
Db 1 QDWSSFQNKHIDYPETSNPNAYCDLMQRR-NLNPTKCKTRNTFVHVSPEIQOVCGS 59
| | | : | : | : | : | : | : | : | : | : | : | : | : |

QY 53 --TGVINNVILSTRFQLNTCTRSIT--PRCPYSSRRTETNYICKENQYVPVHF 104
| | | : | : | : | : | : | : | : | : | : | : | : | : |
Db 60 GGTHYEDNLSDNESFDLTDCKNVGSTAPSSCKYNGTGTGKRIRIACENNQPVHF 114
| | | : | : | : | : | : | : | : | : | : | : | : | : |

RESULT 10
NRPRH
pancreatic ribonuclease (EC 3.1.27.5) - pronghorn (tentative sequence)
N;Alternate names: RNase 1; RNase A
C;Species: Antilocapra americana (pronghorn)
C;Date: 28-Feb-1981 #sequence_revision 28-Feb-1981 #text_change 31-Mar-2000
C;Accession: A00813
R;Beintema, J.J.; Gastra, W.; Munnikema, J.
J. Mol. Evol. 13, 305-316, 1979
A;Title: Primary structure of pronghorn pancreatic ribonuclease: close relationship
A;Reference number: A00813; MUID:80075014; PMID:513141
A;Residues: 1-119 <ZHA>

```

RESULT 10
NRPRH
pancreatic ribonuclease (EC 3.1.27.5) - pronghorn (tentative sequence)
N:Alternate names: RNase A
C:Species: Antilocapra americana (pronghorn)
C>Date: 28-Feb-1981 #sequence_revision 28-Feb-1981 #text_change 31-Mar-2000
C:Accession: A00813
R:Beintema, J.J.; Gastra, W.; Munnikama, J.
J. Mol. Evol. 13, 305-316, 1979
A:Title: Primary structure of pronghorn pancreatic ribonuclease: close relationship between
A:Reference number: A00813; PMID:80075014; PMID:513141
A:Accession: A00813
A:Molecule type: protein
A:Residues: 1-124 <BEI>
C:Superfamily: pancreatic ribonuclease
C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F:12,41,119/Active site: His, Lys, His #status predicted
F:26-84,40-95,68-110,65-72/Disulfide bonds: #status predicted
F:34/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental

Query Match          20.2%; Score 122.5; DB 1; Length 124;
Best Local Similarity 30.3%; Pred. No. 3.3e-05;
Matches 36; Conservative 18; Mismatches 42; Indels 23; Gaps 7;

QY      5 ATFOQHGIINTPI-----ICNTIMDNHYIVGGCKRVNTFISSATTVKAICTGVNM 58
         ||::| : |::| : |::| : |::| : |::| : |::| : |::| : |::| :

```

```
Db 6 AKFERQHIDSNPSSVSSSYCHNOMKSR-NLTQGRCKPNTFTVHESLADVOAVCS---QK 61
Qy 59 NVL-----STTRFQNLNCTRTSITPRP-CPYSSRTETNYICVKE-NQY-PVHF 104
Db 62 NVACKNGOTNCYQSYSTWSITDCRETGSSKYPNCAYKTTQAKKHIIVACEGPNYPVPHY 120

RESULT 11
NRKR
pancreatic ribonuclease (EC 3.1.1.27.5) - red kangaroo
N:Alternate names: RNase 1; RNase A
C:Species: Macropus rufus, Megaleia rufa (red kangaroo)
C:Date: 30-Nov-1980 #sequence_revision 30-Nov-1980 #text_change 04-Oct-1996
C:Accession: A00833
R:Gaaster, W.; Welling, G.W.; Beintema, J.J.
Eur. J. Biochem. 86, 209-217, 1978
A:Title: The amino-acid sequence of kangaroo pancreatic ribonuclease.
A:Reference number: A00833; MUID:78190621; PMID:658039
A:Accession: A00833
A:Molecule type: protein
A:Residues: 1-122 <GAA>
C:Superfamily: pancreatic ribonuclease
C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F:11.40.117/Active site: His, Lys, His #status predicted
F:25-83.39-94.57-109.64-71/Disulfide bonds: #status predicted
F:61/Binding site: carbohydrate (Asn) (covalent) #status absent

Query Match 20.1%; Score 122; DB 1; Length 122;
Best Local Similarity 30.7%; Pred. No. 3.6e-05;
Matches 35; Conservative 16; Mismatches 45; Indels 10; Gaps 6;

Qy 7 FQKH-----INTPIICNTIMDNINIVYGCKRVNTFISSATTVKAIC----- 52
Db 7 FORQMDTHTSHASSNYCNLMKAR-DWTSGRCPNLTFTIHPKSVDAVCHQENVTCK 65

Qy 53 TGVINNVLSITRFQNLNCTRTSITPRP-CPYSSRTETNYICVKENQY-PVHF 104
Db 66 NGRTNC-YKSNRSLTITCROTGASKYPNCQYETSNLKQIIVACEGQYVPVHF 118

RESULT 12
NRKU
pancreatic ribonuclease (EC 3.1.1.27.5) - nutria (tentative sequence)
N:Alternate names: RNase 1; RNase A
C:Species: Myocastor coypus (nutria, coypu)
C:Date: 24-Apr-1984 #sequence_revision 30-Sep-1988 #text_change 31-Mar-2000
C:Accession: A00822
R:van den Berg, A.; van den Hende-Timmer, L.; Beintema, J.J.
Biochim. Biophys. Acta 453, 400-409, 1976
A:Title: Isolation, properties and primary structure of coypu and chinchilla pancreatic
A:Reference number: A0612; MUID:77065676; PMID:999896
A:Accession: A00822
A:Molecule type: protein
A:Residues: 1-128 <VAN>
C:Superfamily: pancreatic ribonuclease
C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F:12.41.119/Active site: His, Lys, His #status predicted
F:26-84.40-95.58-110.65-72/Disulfide bonds: #status predicted
F:34/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 19.9%; Score 120.5; DB 1; Length 128;
Best Local Similarity 31.6%; Pred. No. 5.4e-05;
Matches 37; Conservative 15; Mismatches 42; Indels 23; Gaps 7;

Qy 7 FQKH-----INTPIICNTIMDNINIVYGCKRVNTFISSATTVKAICTGVINNV 60
Db 8 FORQMDSRGSPSTPNVFNEMKSR-NNTQGRCKPNTFTVHESLADVOAVC---FQKNV 63

Qy 61 L-----STTRFQNLNCTRTSITPRP-CPYSSRTETNYICVKE-NQY-PVHF 104
Db 64 LCKNGOTNCYQSNMHIIDCHRTVNSDYPNCSYRTSQEKSIVACEGPNYPVPHF 120
```

RESULT 13

```
NRMS
pancreatic ribonuclease (EC 3.1.1.27.5) precursor - mouse
N:Alternate names: RNase 1; RNase A
C:Species: Mus musculus (house mouse)
C:Date: 30-Nov-1980 #sequence_revision 13-Mar-1997 #text_change 18-Jun-1999
C:Accession: A34090; S22598; A00830
R:Schueller, C.; Nijssen, H.M.J.; Kok, R.; Beintema, J.J.
Mol. Biol. Evol. 7, 29-44, 1990
A:Title: Evolution of nucleic acids coding for ribonucleases: the mRNA sequence of mouse
A:Reference number: A34090; MUID:90136034; PMID:2299980
A:Accession: A34090
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-149 <SCH>
A:Cross-references: GB:M27814; NID:g200762; PIDN:AAA40060.1; PID:g200763
R:Samuelson, L.C.; Wiebauer, K.; Howard, G.; Schmid, R.M.; Koeplin, D.; Meisler, M.H.
Nucleic Acids Res. 19, 6935-6941, 1991
A:Title: Isolation of the murine ribonuclease gene Rib-1: structure and tissue specific
A:Reference number: S22598; MUID:92107684; PMID:1840677
A:Accession: S22598
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-149 <SAM>
A:Cross-references: EMBL:X60103; NID:g53981; PIDN:CAA42697.1; PID:g53982
R:Lenstra, J.A.; Beintema, J.J.
Eur. J. Biochem. 96, 399-408, 1979
A:Title: The amino acid sequence of mouse pancreatic ribonuclease.
A:Reference number: A00830; MUID:80024269; PMID:556267
A:Accession: A00830
A:Molecule type: protein
A:Residues: 26-149 <LEN>
C:Superfamily: pancreatic ribonuclease
C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F:1-25/Domain: signal sequence #status predicted <SIG>
F:26-149/Product: pancreatic ribonuclease #status experimental <MAT>
F:37.66.144/Active site: His, Lys, His #status predicted
F:51-109.65-120.83-135.90-97/Disulfide bonds: #status predicted
F:62.87/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 19.9%; Score 120.5; DB 1; Length 149;
Best Local Similarity 30.8%; Pred. No. 6.3e-05;
Matches 36; Conservative 16; Mismatches 42; Indels 23; Gaps 7;

Qy 7 FQKH-----INTPIICNTIMDNINIVYGCKRVNTFISSATTVKAICTGVINNV 60
Db 33 FORQMDPDGSSINSPTYCNQMKRR-DWTGSCRPVNTFVHEPLADVOAVCS---QENV 88

Qy 61 L-----STTRFQNLNCTRTSITPRP-CPYSSRTETNYICVKE-NQY-PVHF 104
Db 89 TCKNRKSNCKYKSSSALHITDCHLKSGSKYPNCYDKYKTQYQKHIIIVACEGPNYPVPHF 145

RESULT 14
A43825
angiogenin - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: S29834; A43825
R:Bond, M.D.; Strydom, D.J.; Vallee, B.L.
Biochim. Biophys. Acta 1162, 177-186, 1993
A:Title: Characterization and sequencing of rabbit, pig and mouse angiogenins: discernme
A:Reference number: S29833; MUID:93192291; PMID:8448182
A:Accession: S29834
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-123 <BON>
A:Note: this sequence was submitted to the Protein Sequence Database, December 1992
C:Superfamily: pancreatic ribonuclease

Query Match 19.7%; Score 119.5; DB 1; Length 123;
Best Local Similarity 39.5%; Pred. No. 6.5e-05;
Matches 30; Conservative 6; Mismatches 35; Indels 5; Gaps 2;
```

Qy 34 CKRVNTFISSATTVAICTG-----VINNNVLSTTRFOLNTCTRTSITPR-PCPYSSRTE 88
Db 39 CKRVNTFIHGTRNDIKALCNDKNGEPYNNFRSRKSPFOITTCCKHKGGSNRPPCGYRATAG 98
Qy 89 TNYICVKCENQYPVHF 104
Db 99 FRTIACACENGLPVHF 114

RESULT 15
NRGPB
pancreatic ribonuclease (EC 3.1.27.5) B - guinea pig (tentative sequence)
N:Alternate names: RNase IB
C:Species: Cavia porcellus (guinea pig)
C:Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 31-Mar-2000
C:Accession: A00826
R:van den Berg, A.; van den Hende-Timmer, L.; Hofsteenge, J.; Gastra, W.; Beintema, J.J.
Eur. J. Biochem. 75, 91-100, 1977
A:Title: Guinea pig pancreatic ribonucleases. Isolation, properties, primary structure and
A:Reference number: A91247; MUID:77185023; PMID:862624
A:Accession: A00826
A:Molecule type: protein
A:Residues: 1-128 <VAN>
A:Note: 64-Pro was also found
C:Superfamily: pancreatic ribonuclease
C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F:12.41.119/Active site: His, Lys, His #status predicted
F:21.34/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:26-84,40-95,58-110,65-72/disulfide bonds: #status predicted

Query Match 19.5%; Score 118.5; DB 1; Length 128;
Best Local Similarity 31.6%; Pred. No. 8.5e-05;
Matches 37; Conservative 14; Mismatches 43; Indels 23; Gaps 6;

Qy 7 FQKH-----INTPLICNTIMDNIYVCGQCKRVNTFISSATTVAICTGVINNV 60
Db 8 FQOHMDPEGSPSNSSNYCNVMIR-NMTQGRCKPVNTFVHESLADYQAVC---FQKNV 63
Qy 61 L-----STTRFOLNTCTRTSITPR-CPYSSRTEITNYICVKCENQ--YPVHF 104
Db 64 LCKNGQTCYQYSRMRITDCRVTSSSKFPNCYSRMSQAQKSIIVACEGDPYPVHP 120

Search completed: January 22, 2004, 12:03:22
Job time : 13.4719 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 22, 2004, 12:01:30 : Search time 13.3034 Seconds
(without alignments)
353.031 Million cell updates/sec

Title: US-09-622-613C-17

Perfect score: 607

Sequence: 1 MQWATFQKHINTPIICN.....ICVKENQVPHFAGIGRCP 111

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A COMB.pcp.*
2: /cgn2_6/ptodata/1/iaa/5B COMB.pcp.*
3: /cgn2_6/ptodata/1/iaa/6A COMB.pcp.*
4: /cgn2_6/ptodata/1/iaa/6B COMB.pcp.*
5: /cgn2_6/ptodata/1/iaa/PTUS COMB.pcp.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	588.5	97.0	111	2	US-08-891-848-12
2	588.5	97.0	111	3	US-08-875-811-8
3	284.5	46.9	104	1	US-08-467-955-2
4	279.5	46.0	105	3	US-08-875-811-39
5	279.5	46.0	355	3	US-08-875-811-41
6	279.5	46.0	358	3	US-08-875-811-51
7	277.5	45.7	104	3	US-09-394-268-1
8	277.5	45.7	104	4	US-09-687-748-1
9	277.5	45.7	112	3	US-08-875-811-32
10	277.5	45.7	129	3	US-08-875-811-63
11	277.5	45.7	251	3	US-08-875-811-59
12	277.5	45.7	254	3	US-08-875-811-61
13	277.5	45.7	355	3	US-08-875-811-49
14	277.5	45.7	355	3	US-08-875-811-57
15	277.5	45.7	355	3	US-08-875-811-64
16	277.5	45.7	366	3	US-08-875-811-55
17	277.5	45.7	379	3	US-08-875-811-43
18	274.5	45.2	104	1	US-08-283-971-1
19	274.5	45.2	104	1	US-07-921-619-1
20	274.5	45.2	104	1	US-08-467-955-1
21	274.5	45.2	104	2	US-08-891-848-13
22	272.5	44.9	104	3	US-08-875-811-1
23	272.5	44.9	104	3	US-09-394-268-2
24	272.5	44.9	104	4	US-09-071-672-1
25	272.5	44.9	104	4	US-09-687-748-2
26	272.5	44.9	105	3	US-08-875-811-26
27	272.5	44.9	106	3	US-08-875-811-28

28 272.5 44.9 107 3 US-08-875-811-30
29 271.5 44.7 105 3 US-08-875-811-24
30 268.5 44.2 358 3 US-08-875-811-45
31 268.5 44.2 365 3 US-08-875-811-53
32 250.5 41.3 107 3 US-08-875-811-20
33 239.5 39.5 111 3 US-08-875-811-22
34 236 38.9 114 3 US-09-223-118-3
35 232.5 38.3 360 3 US-08-875-811-47
36 227 37.4 114 3 US-09-223-118-2
37 226 37.2 114 3 US-09-223-118-1
38 225 33.9 114 3 US-09-223-118-4
39 206 33.9 83 3 US-08-875-811-2
40 206 33.9 83 4 US-09-071-672-3
41 163 26.9 169 1 US-08-441-629-2
42 163 26.9 169 3 US-08-776-207-2
43 163 26.9 169 4 US-09-507-773-2
44 163 26.9 169 5 PCT-US95-09172-2
45 124.5 20.5 125 6 5171845-2

ALIGNMENTS

RESULT 1

US-08-891-848-12
; Sequence 12, Application US/08891848
; Patent No. 5955073
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Youle, Richard J.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Nicholls, Peter J.
; TITLE OF INVENTION: Selective RNase Cytotoxic Reagents
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/08/891,848
; FILING DATE: No. 5955073 yet assigned
; CLASSIFICATION: 530
; PRIOR APPLICATION NUMBER: US 08/125,462
; FILING DATE: 22-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/014,082
; FILING DATE: 04-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/779,195
; FILING DATE: 22-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/510,696
; FILING DATE: 20-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 015280-110310US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 111 amino acids
; TYPE: amino acid

Sequence 30, Appl
Sequence 24, Appl
Sequence 45, Appl
Sequence 53, Appl
Sequence 20, Appl
Sequence 22, Appl
Sequence 3, Appl
Sequence 47, Appl
Sequence 2, Appl
Sequence 4, Appl
Sequence 2, Appl
Sequence 3, Appl
Sequence 2, Appl
Sequence 2, Appl
Sequence 2, Appl
Patent No. 5171845

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; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..111
; OTHER INFORMATION: /note= "Frog Lectin from Rana
; US-08-891-848-12
; OTHER INFORMATION: /note= "Frog Lectin from Rana
; catesbeiana"
; US-08-875-811-8
;
Query Match 97.0%; Score 588.5; DB 2; Length 111;
Best Local Similarity 98.2%; Pred. No. 5e-61;
Matches 109; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

Qy 2 QNWATFOOKHIIINTPII-CNTIMDNIIYVGGCKRVNTFTLISSATTVKAICTGVINNV 60
Db 1 ENWATFOOKHIIINTPIINCNTIMDNIIYVGGCKRVNTFTLISSATTVKAICTGVINNV 60
Qy 61 LSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRCP 111
Db 61 LSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRCP 111

RESULT 2
US-08-875-811-8
; Sequence 8, Application US/08875811
; Patent No. 6045793
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Boque, Luis
; APPLICANT: Wlodawer, Alexander
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875.811
; FILING DATE: 19-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/02588
; FILING DATE: 19-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/011,800
; FILING DATE: 21-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Faria, Susan K.
; REGISTRATION NUMBER: 41,739
; REFERENCE/DOCKET NUMBER: 015280-244100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 111 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..111

;
Query Match 97.0%; Score 588.5; DB 3; Length 111;
Best Local Similarity 98.2%; Pred. No. 5e-61;
Matches 109; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

Qy 2 QNWATFOOKHIIINTPII-CNTIMDNIIYVGGCKRVNTFTLISSATTVKAICTGVINNV 60
Db 1 ENWATFOOKHIIINTPIINCNTIMDNIIYVGGCKRVNTFTLISSATTVKAICTGVINNV 60
Qy 61 LSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRCP 111
Db 61 LSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRCP 111

RESULT 3
US-08-467-955-2
; Sequence 2, Application US/08467955
; Patent No. 5728805
; GENERAL INFORMATION:
; APPLICANT: Ardeit Ph.D. Wojciech J.
; TITLE OF INVENTION: PHARMACEUTICALS AND METHOD FOR MAKING THEM
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Mark H. Jay, P.A.
; STREET: P.O. Box E
; CITY: Short Hills
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07078-0383
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,955
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/178,118
; FILING DATE: 06-APR-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/436,141
; FILING DATE: 13-NOV-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/814,332
; FILING DATE: 03-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/283,970
; FILING DATE: 01-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Jay, Mark H.
; REGISTRATION NUMBER: 27507
; REFERENCE/DOCKET NUMBER: 5007 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-912-9066
; TELEFAX: 201-912-0442
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 104 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: N
; ANTI-SENSE: N
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Rana pipiens
```


DEVELOPMENTAL STAGE: Oocyte
US-08-467-955-2

Query Match 46.9%; Score 284.5; DB 1; Length 104;
Best Local Similarity 49.5%; Pred. No. 9.1e-26;
Matches 55; Conservative 16; Mismatches 31; Indels 9; Gaps 4;
Oy 2 QNWATFOQKHINT-PIICNTIMDNIIYVGQCKRVNTFISSATTVKAICTGVI-NM 59
Db 1 EDWLTFOQKHINTNRDVCNNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIASKN 56
Oy 60 VLSTTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
Db 57 VLTTSEFYLSDC---NVTSRPCKYKLLKSTNKFVTCENQAPVHFVGVGRC 104

RESULT 4
US-08-875-811-39
; Sequence 39, Application US/08875811
; Patent No. 6045793
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Boque, Lluís
; APPLICANT: Wlodawer, Alexander
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,811
; FILING DATE: 19-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/02588
; FILING DATE: 19-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/011,800
; FILING DATE: 21-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Faria, Susan K.
; REGISTRATION NUMBER: 41,739
; REFERENCE/DOCKET NUMBER: 015280-244100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 105 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-875-811-39

Query Match 46.0%; Score 279.5; DB 3; Length 105;
Best Local Similarity 49.1%; Pred. No. 3.5e-25;
Matches 55; Conservative 16; Mismatches 32; Indels 9; Gaps 4;
Oy 1 MQNWATFOQKHINT-PIICNTIMDNIIYVGQCKRVNTFISSATTVKAICTGVI-NM 58
Db 1 MEDWLTFOQKHINTNRDVCNNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIASK 56
Oy 59 NVLSTTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
Db 307 NVLTTSEFYLSDC---NVTSRPCKYKLLKSTNKFVTCENQAPVHFVGVGSC 355

RESULT 6
US-08-875-811-51
; Sequence 51, Application US/08875811
; Patent No. 6045793
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Boque, Lluís

Db 57 NVLTTSEFYLSDC---NVTSRPCKYKLLKSTNKFVTCENQAPVHFVGVGSC 105

RESULT 5
US-08-875-811-41
; Sequence 41, Application US/08875811
; Patent No. 6045793
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Boque, Lluís
; APPLICANT: Wlodawer, Alexander
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,811
; FILING DATE: 19-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/02588
; FILING DATE: 19-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/011,800
; FILING DATE: 21-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Faria, Susan K.
; REGISTRATION NUMBER: 41,739
; REFERENCE/DOCKET NUMBER: 015280-244100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-875-811-41

Query Match 46.0%; Score 279.5; DB 3; Length 355;
Best Local Similarity 49.1%; Pred. No. 1.6e-24;
Matches 55; Conservative 16; Mismatches 32; Indels 9; Gaps 4;
Oy 1 MQNWATFOQKHINT-PIICNTIMDNIIYVGQCKRVNTFISSATTVKAICTGVI-NM 58
Db 251 MEDWLTFOQKHINTNRDVCNNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIASK 306
Oy 59 NVLSTTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
Db 307 NVLTTSEFYLSDC---NVTSRPCKYKLLKSTNKFVTCENQAPVHFVGVGSC 355

RESULT 6
US-08-875-811-51
; Sequence 51, Application US/08875811
; Patent No. 6045793
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Boque, Lluís

```
; APPLICANT: Wlodawer, Alexander
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,811
; FILING DATE: 19-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/02588
; FILING DATE: 19-FEB-1997
; PRIOR APPLICATION NUMBER: US 60/011,800
; FILING DATE: 21-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Paris, Susan K.
; REGISTRATION NUMBER: 41,739
; REFERENCE/DOCKET NUMBER: 015280-244100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 358 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-875-811-51

Query Match 46.0%; Score 279.5; DB 3; Length 358;
Best Local Similarity 49.1%; Pred. No. 1.6e-24;
Matches 55; Conservative 16; Mismatches 32; Indels 9; Gaps 4;

Qy 1 MNWATFQOKHIINT-PIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVI-NM 58
Db 1 MEDWLTFOKKHINTNRDVEDCDNIMSTNLF---HCKDKNTFIYSRPEPVKAICKGIIASK 56

Qy 59 NVLSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRC 110
Db 57 NVLTTFEYLSDC---NVTSRPCKYKLLKSTNKFVTCENQAPVHFVGVGSC 105

RESULT 7
US-09-394-268-1
; Sequence 1, Application US/09394268
; Patent No. 6175003
; GENERAL INFORMATION:
; APPLICANT: Saxena, Shailendra K
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING RIBONUCLEASES AND METHODS OF
; MAKING THEM
; FILE REFERENCE: 5013
; CURRENT APPLICATION NUMBER: US/09/394,268
; CURRENT FILING DATE: 1999-09-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 104
; TYPE: PRT
; ORGANISM: Rana pipiens
US-09-394-268-1

Query Match 45.7%; Score 277.5; DB 3; Length 104;
Best Local Similarity 49.1%; Pred. No. 1.6e-24;
Matches 55; Conservative 16; Mismatches 32; Indels 9; Gaps 4;

Qy 1 MNWATFQOKHIINT-PIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVI-NM 58
Db 1 MEDWLTFOKKHINTNRDVEDCDNIMSTNLF---HCKDKNTFIYSRPEPVKAICKGIIASK 56

Qy 59 NVLSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRC 110
Db 57 NVLTTFEYLSDC---NVTSRPCKYKLLKSTNKFVTCENQAPVHFVGVGSC 105

RESULT 8
US-09-687-748-1
; Sequence 1, Application US/09687748
; Patent No. 6423515
; GENERAL INFORMATION:
; APPLICANT: Saxena, Shailendra K
; TITLE OF INVENTION: METHODS OF MAKING NUCLEIC ACIDS ENCODING RIBONUCLEASES
; FILE REFERENCE: 5013 US 01
; CURRENT APPLICATION NUMBER: US/09/687,748
; CURRENT FILING DATE: 2000-10-14
; PRIOR APPLICATION NUMBER: 09/394,268
; PRIOR FILING DATE: 1999-09-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 104
; TYPE: PRT
; ORGANISM: Rana pipiens
US-09-687-748-1

Query Match 45.7%; Score 277.5; DB 4; Length 104;
Best Local Similarity 49.5%; Pred. No. 5.9e-25;
Matches 55; Conservative 15; Mismatches 32; Indels 9; Gaps 4;

Qy 2 QNWATFQOKHIINT-PIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVI-NMN 59
Db 1 QDWLTFOKKHINTNRDVEDCDNIMSTNLF---HCKDKNTFIYSRPEPVKAICKGIIASKN 56

Qy 60 VLSTTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRC 110
Db 57 VLTTFEYLSDC---NVTSRPCKYKLLKSTNKFVTCENQAPVHFVGVGSC 104

Best Local Similarity 49.5%; Pred. No. 5.9e-25;
Matches 55; Conservative 15; Mismatches 32; Indels 9; Gaps 4;
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; APPLICATION NUMBER: WO PCT/US97/02588
; FILING DATE: 19-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/011,800
; FILING DATE: 21-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Faris, Susan K.
; REGISTRATION NUMBER: 41,739
; REFERENCE/DOCKET NUMBER: 015280-244100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-875-811-32

Query Match          45.7%; Score 277.5; DB 3; Length 112;
Best Local Similarity 49.1%; Pred. No. 6.5e-25;
Matches 55; Conservative 15; Mismatches 33; Indels 9; Gaps 4;

Qy 1 MQNWATFOQKHINT-PIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVI-NM 58
Db 8 MSDWLTFOQKHITNTRDVDCDNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIASK 63

Qy 59 NVLSTTRFQNTCTRTSITPRPCYSSTRTETNYICVKCENQYPVHFAGIGRC 110
Db 64 NVLTSEFVLSDC---NVTSPCKYKLLKSTNKFVTCENQAPVHFVGVGSC 112

RESULT 10
US-08-875-811-63
; Sequence 63, Application US/08875811
; Patent No. 6045793
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Boque, Lluís
; APPLICANT: Wlodawer, Alexander
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,811
; FILING DATE: 19-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/02588
; FILING DATE: 19-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/011,800
; FILING DATE: 21-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Faris, Susan K.
; REGISTRATION NUMBER: 41,739
; REFERENCE/DOCKET NUMBER: 015280-244100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
```

```
; INFORMATION FOR SEQ ID NO: 63:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 129 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-875-811-63

Query Match          45.7%; Score 277.5; DB 3; Length 129;
Best Local Similarity 49.5%; Pred. No. 7.7e-25;
Matches 55; Conservative 15; Mismatches 32; Indels 9; Gaps 4;

Qy 2 QNWATFOQKHINT-PIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVI-NMN 59
Db 26 QDWLTFOQKHITNTRDVDCDNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIASKN 81

Qy 60 VLSTTRFQNTCTRTSITPRPCYSSTRTETNYICVKCENQYPVHFAGIGRC 110
Db 82 VLTTSEFVLSDC---NVTSPCKYKLLKSTNKFVTCENQAPVHFVGVGSC 129

RESULT 11
US-08-875-811-59
; Sequence 59, Application US/08875811
; Patent No. 6045793
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Boque, Lluís
; APPLICANT: Wlodawer, Alexander
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,811
; FILING DATE: 19-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/02588
; FILING DATE: 19-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/011,800
; FILING DATE: 21-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Faris, Susan K.
; REGISTRATION NUMBER: 41,739
; REFERENCE/DOCKET NUMBER: 015280-244100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-875-811-59

Query Match          45.7%; Score 277.5; DB 3; Length 251;
Best Local Similarity 49.1%; Pred. No. 1.7e-24;
Matches 55; Conservative 15; Mismatches 33; Indels 9; Gaps 4;
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Oy 1 MONWATFOOKHIINT-PIICNTIMDNNIYVGGCKRVNTFISSATTVKAICTGVI-NM 58
Db 147 MSDWLTFOKKHITNTRDVCNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIITASK 202

Oy 59 NVLSTTRFQNLCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
Db 203 NVLTTSFYLSDC---NVTSRPKYKLLKSTNKFVCVTENQAPVHFVGVGSC 251

RESULT 12
US-08-875-811-61
; Sequence 61, Application US/08875811
; Patent No. 6045793
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Boque, Lluís
; APPLICANT: Wlodawer, Alexander
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875.811
; FILING DATE: 19-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/02588
; FILING DATE: 19-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/011.800
; FILING DATE: 21-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Paris, Susan K.
; REGISTRATION NUMBER: 41,739
; REFERENCE/DOCKET NUMBER: 015280-244100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 61:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 254 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-875-811-61

Query Match 45.7%; Score 277.5; DB 3; Length 254;
Best Local Similarity 49.1%; Pred. No. 1.8e-24;
Matches 55; Conservative 15; Mismatches 33; Indels 9; Gaps 4;

Oy 1 MONWATFOOKHIINT-PIICNTIMDNNIYVGGCKRVNTFISSATTVKAICTGVI-NM 58
Db 1 MSDWLTFOKKHITNTRDVCNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIITASK 56

Oy 59 NVLSTTRFQNLCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
Db 57 NVLTTSFYLSDC---NVTSRPKYKLLKSTNKFVCVTENQAPVHFVGVGSC 105

RESULT 13
US-08-875-811-49
; Sequence 49, Application US/08875811
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; Patent No. 6045793
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Boque, Lluís
; APPLICANT: Wlodawer, Alexander
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875.811
; FILING DATE: 19-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/02588
; FILING DATE: 19-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/011.800
; FILING DATE: 21-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Paris, Susan K.
; REGISTRATION NUMBER: 41,739
; REFERENCE/DOCKET NUMBER: 015280-244100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-875-811-49

Query Match 45.7%; Score 277.5; DB 3; Length 355;
Best Local Similarity 49.1%; Pred. No. 2.7e-24;
Matches 55; Conservative 15; Mismatches 33; Indels 9; Gaps 4;

Oy 1 MONWATFOOKHIINT-PIICNTIMDNNIYVGGCKRVNTFISSATTVKAICTGVI-NM 58
Db 251 MSDWLTFOKKHITNTRDVCNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIITASK 306

Oy 59 NVLSTTRFQNLCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 110
Db 307 NVLTTSFYLSDC---NVTSRPKYKLLKSTNKFVCVTENQAPVHFVGVGSC 355

RESULT 14
US-08-875-811-57
; Sequence 57, Application US/08875811
; Patent No. 6045793
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Boque, Lluís
; APPLICANT: Wlodawer, Alexander
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 22, 2004, 12:01:21 ; Search time 27.4382 Seconds
(without alignment)
1043.940 Million cell updates/sec

Title: US-09-622-613C-17

Perfect score: 607

Sequence: 1 MQNWATPQKHINTPIICN.....ICVKCNQYVHPFAGIGRCP 111

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 23:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	591.5	97.4	133	13	Q9PWR7
2	560.5	92.3	133	13	Q98SM0
3	487.5	80.3	132	13	Q98SM2
4	478.5	78.8	133	13	Q98SL9
5	471.5	77.7	133	13	Q98SL8
6	448.5	73.9	132	13	Q98SM1
7	376	61.9	132	13	Q9DF78
8	281.5	46.4	127	13	Q918V8
9	277.5	45.7	127	13	Q8UVX5
10	246	40.5	129	13	Q9DFY6
11	229.5	37.6	128	13	Q9DFY8
12	226.5	37.3	128	13	Q9DFY7
13	217.5	35.8	128	13	Q9DFY5
14	163	26.9	169	13	Q9W738
15	131	21.6	170	6	Q9BEC1
16	126	20.8	150	11	Q8VD94

17	125.5	20.7	163	6	Q9BDC2
18	124.5	20.5	116	6	Q9TVC0
19	124	20.4	150	11	Q8VD88
20	122.5	20.2	144	6	Q9BH14
21	120.5	19.9	149	11	Q8K2T2
22	120.5	19.9	149	11	Q8CGG3
23	120	19.8	150	11	Q8VD92
24	116.5	19.2	152	11	Q8VD89
25	115.5	19.0	119	6	Q9TV13
26	114.5	18.9	124	6	Q95NE6
27	112.5	18.5	148	11	Q8C7E4
28	112.5	18.5	149	11	Q8VD95
29	112	18.5	134	6	Q9BDB9
30	111.5	18.4	152	11	Q8VD84
31	111.5	18.4	156	6	Q8S005
32	111	18.3	148	11	Q8C663
33	110.5	18.2	119	6	Q9TV28
34	110.5	18.2	119	6	Q9TV10
35	110.5	18.2	124	6	Q9TSP2
36	109.5	18.0	142	6	Q9BEC3
37	109.5	18.0	156	6	Q8S006
38	109	18.0	124	6	Q9BEC2
39	108.5	17.9	156	6	Q8SQ08
40	108.5	17.9	156	6	Q8SQ07
41	107.5	17.7	152	11	Q8VD90
42	106.5	17.5	116	6	Q97933
43	106.5	17.5	149	11	Q8VD93
44	105.5	17.4	116	6	Q97934
45	105.5	17.4	119	6	Q9TSQ6

ALIGNMENTS

RESULT 1

Q9PWR7 ID Q9PWR7 PRELIMINARY; PRT; 133 AA.

AC Q9PWR7; 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Ribonuclease precursor.
 GN RCR.
 OS Rana catesbeiana (Bull frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
 NCBI_TaxID=8400;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=98165825; PubMed=9497370;
 RA Huang H.C., Wang S.C., Leu Y.J., Lu S.C., Liao Y.D.;
 RT "The Rana catesbeiana rcr gene encoding a cytotoxic ribonuclease.
 RT Tissue distribution, cloning, purification, cytotoxicity, and active
 RT residues for RNase activity";
 RL J. Biol. Chem. 273:6395-6401(1998).
 DR EMBL; AF039104; AAD10702.1; -;
 DR HSSP; P11916; 1BC4
 DR InterPro; IPR001427; RNaseA.
 DR Pfam; PF00074; rnasea; 1.
 DR ProDom; PD000535; RNaseA; 1.
 DR SMART; SM00092; RNase PC; 1.
 DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
 KW SIGNAL.
 FT SIGNAL.
 FT CHAIN 1 22 POTENTIAL.
 SQ SEQUENCE 133 AA; 14762 MW; A7D62594F7D16F0C CRC64;
 23 133 RIBONUCLEASE.

Query Match 97.4%; Score 591.5; DB 13; Length 133;
 Best Local Similarity 99.1%; Pred.No. 4.5e-60;
 Matches 110; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 2 QNWATPQKHINTPII-CNTIMDNNIYVGGCKRVNTPFISSATTVTKAICTGVINMV 60


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ID Q98SL8 PRELIMINARY; PRT; 133 AA.
AC Q98SL8;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE RNase A-type ribonuclease rc218 precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21539506; PubMed=11683320;
RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT "Rapid diversification of RNase A superfamily ribonuclease from the
RT bullfrog, Rana catesbeiana";
RL J. Mol. Evol. 53:31-38(2001).
DR EMBL; AF351211; AAK30257.1; -.
DR HSSP; P11916; 1BC4.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_Pc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL
SQ SEQUENCE 1 22 POTENTIAL.
Query Match 77.7%; Score 471.5; DB 13; Length 133;
Best Local Similarity 76.6%; Pred. No. 2.6e-46;
Matches 85; Conservative 13; Mismatches 12; Indels 1; Gaps 1;

Qy 2 QNWATFOOKHIINTPII-CNTIMDNIIYVGQCKRVNTFISSATTVKAICTGVINNV 60
Db 23 QNWATFOOHIINTSSINCNSIMNSLIYVGQCKKVNFTFIASATTVKIGCSGVTDKV 82

Qy 61 LSTTRFQNLCTRTSITPRPCPSYSSRTETNYICVKCENQYPVHFAGIGRC 111
Db 83 LSTKFKQLDICTRIFITPRPCPSYSSRTETNYICVKCENQYPVHFAGIGQCP 133

RESULT 6
Q98SM1 PRELIMINARY; PRT; 132 AA.
AC Q98SM1;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE RNase A-type ribonuclease rc204 precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21539506; PubMed=11683320;
RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT "Rapid diversification of RNase A superfamily ribonuclease from the
RT bullfrog, Rana catesbeiana";
RL J. Mol. Evol. 53:31-38(2001).
DR EMBL; AF351208; AAK30254.1; -.
DR HSSP; P11916; 1BC4.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_Pc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL
SQ SEQUENCE 1 22 POTENTIAL.
Query Match 73.9%; Score 448.5; DB 13; Length 132;
Best Local Similarity 78.2%; Pred. No. 1.1e-43;

Qy 2 QNWATFOOKHIINTPII-CNTIMDNIIYVGQCKRVNTFISSATTVKAICTGVINNV 60
Db 23 QNWATFOOHIINTSSINCNSIMNSLIYVGQCKKVNFTFIASATTVKIGCSGVTDKV 82

Qy 61 LSTTRFQNLCTRTSITPRPCPSYSSRTETNYICVKCENQYPVHFAGIGRC 111
Db 83 LSTKFKQLDICTRIFITPRPCPSYSSRTETNYICVKCENQYPVHFAGIGQCP 133

RESULT 7
Q9DF78 PRELIMINARY; PRT; 132 AA.
AC Q9DF78;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-OCT-2001 (TReMBLrel. 18, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE RC-RNaseL1 ribonuclease precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Liver;
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RT "Purification and cloning of cytotoxic ribonucleases from Rana
RT catesbeiana (bullfrog).";
RL Nucleic Acids Res. 28:4097-4104(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX TISSUE=Liver;
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF288642; AAG30414.2; -.
DR HSSP; P11916; 1BC4.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_Pc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL
SQ SEQUENCE 1 21 POTENTIAL.
Query Match 61.9%; Score 376; DB 13; Length 132;
Best Local Similarity 65.8%; Pred. No. 2.3e-35;
Matches 73; Conservative 9; Mismatches 27; Indels 2; Gaps 2;

Qy 2 QNWATFOOKHIINTPII-CNTIMDNIIYVGQCKRVNTFISSATTVKAICTGVI-NMN 59
Db 22 QNWAKFKKHITSSIDCINTMDKAIYIVGCKKERTNTFISSDNVKAICSGVSPDRK 81

Qy 60 VLSTTRFQNLCTRTSITPRPCPSYSSRTETNYICVKCENQYPVHFAGIGRC 110
Db 82 ELSTTSFKLNTCIRDSITPRPCPYHPSPNNKICVKCKQLPVHFVGVGKGC 132

RESULT 8
Q918V8 PRELIMINARY; PRT; 127 AA.
AC Q918V8;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Onconase variant rapLRI precursor.
OS Rana pipiens (Northern leopard frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8404;

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Matches 86; Conservative 7; Mismatches 16; Indels 1; Gaps 1;

Qy 2 QNWATFOOKHIINTPII-CNTIMDNIIYVGQCKRVNTFISSATTVKAICTGVINNV 60
Db 23 QDWPTFOOKHIPSTSSIDCINTMDKDIYIVRGCKKVNFTFISSATTVKAICTGVLSNV 82

Qy 61 LSTTRFQNLCTRTSITPRPCPSYSSRTETNYICVKCENQYPVHFAGIGRC 110
Db 83 LSTTRFQLXXTRFITSRPCPSYSTKETNKICVKCENQYPVHFAGIGKC 132

RESULT 9
Q9DF78 PRELIMINARY; PRT; 132 AA.
AC Q9DF78;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-OCT-2001 (TReMBLrel. 18, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE RC-RNaseL1 ribonuclease precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Liver;
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RT "Purification and cloning of cytotoxic ribonucleases from Rana
RT catesbeiana (bullfrog).";
RL Nucleic Acids Res. 28:4097-4104(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX TISSUE=Liver;
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF288642; AAG30414.2; -.
DR HSSP; P11916; 1BC4.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_Pc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL
SQ SEQUENCE 1 21 POTENTIAL.
Query Match 61.9%; Score 376; DB 13; Length 132;
Best Local Similarity 65.8%; Pred. No. 2.3e-35;
Matches 73; Conservative 9; Mismatches 27; Indels 2; Gaps 2;

Qy 2 QNWATFOOKHIINTPII-CNTIMDNIIYVGQCKRVNTFISSATTVKAICTGVI-NMN 59
Db 22 QNWAKFKKHITSSIDCINTMDKAIYIVGCKKERTNTFISSDNVKAICSGVSPDRK 81

Qy 60 VLSTTRFQNLCTRTSITPRPCPSYSSRTETNYICVKCENQYPVHFAGIGRC 110
Db 82 ELSTTSFKLNTCIRDSITPRPCPYHPSPNNKICVKCKQLPVHFVGVGKGC 132

RESULT 8
Q918V8 PRELIMINARY; PRT; 127 AA.
AC Q918V8;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Onconase variant rapLRI precursor.
OS Rana pipiens (Northern leopard frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8404;

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DR Pfan: PF00074; rnasea; 1.
DR ProDom: PD000535; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
SQ SEQUENCE 169 AA; 18891 MW; D969F3E43B3CE1B8 CRC64;

Query Match
Best Local Similarity 26.9%; Score 163; DB 13; Length 169;
Matches 44; Conservative 10; Mismatches 50; Indels 8; Gaps 6;

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Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
28 QNINAFMEKHIVKEGAETNCNQTIDRNIRF-KNNCKFRNTFIHDTNGKKVKEMCAGIVK 86
Qy 58 MN-VLSTTRFQNLCTRTSITPRP--CPYSSRTETNYICVKCENQYPVHFAG 106
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
87 STFVISKELLPLTDCLLMGRTPARPNCAYNQTRTTGTVINITCENNYPVHFAG 138

RESULT 15
Q9BEC1 PRELIMINARY; PRT; 170 AA.
AC Q9BEC1;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Brain-type ribonuclease ribonuclease precursor (Fragment).
GN RNase B.
OS Tragus javanicus (Lesser Malay chevrotain).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Tragulina;
OC Tragulidae; Tragulus.
OX NCBI_TaxID=9849;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21347458; PubMed=11453981;
RA Breukelman H.J., Jekel P.A., Dubois J.Y., Mulder P.P.M.F.A.,
RA Warmels H.W., Beintema J.J.;
RT "Secretory ribonucleases in the primitive ruminant chevrotain
RT (Tragus javanicus).";
RL Eur. J. Biochem. 268:3890-3897(2001).
CC -!- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
DR EMBL; AJ271299; CAC24723.1; -.
DR HSP; P00656; ILSQ.
DR InterPro; IPR001427; RNaseA.
DR Pfan: PF00074; rnasea; 1.
DR PRINTS; PR00794; RIBONUCLEASE.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase PG; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Endonuclease; Hydrolase; Nuclease; Signal.
FT NON_TER 1 1
FT SIGNAL <1 19 POTENTIAL.
FT CHAIN 20 170 BRAIN-TYPE RIBONUCLEASE RIBONUCLEASE.
SQ SEQUENCE 170 AA; 18832 MW; AB6CE7E1E5549AA0 CRC64;

Query Match
Best Local Similarity 21.6%; Score 131; DB 6; Length 170;
Matches 41; Conservative 17; Mismatches 46; Indels 20; Gaps 7;

Qy 5 ATFOOKHI-----INTPIICNTIMDNIYIVGGCKRVNTFI-ISSATTVKAICT----- 53
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
25 AKFRQRHLDAGNSSINSN-YCNLMKRR-KMTHGRCKPVNTFIHESLEDVKAICSEKNIT 82
Qy 54 ---GVINMVLSTTRFQNLCTRTSITPRP-CPYSSRTETNYICVKCEN--QYPVHFAGI 107
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
83 CKNGQPNCHQNSNT-WNITDCRQCGSKYPNCAKYTSQKYLIVACEGTPSPVHFQGS 141
Qy 108 GRCP 111
Db 142 AVLP 145

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 22, 2004, 12:01:21 ; Search time 27.191 Seconds
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1043.940 Million cell updates/sec

Title: US-09-622-613C-19
Perfect score: 600
Sequence: 1 QNWATFOQKHINTPIICNT.....ICVRCENQYPVHFAGIGRCP 110

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues
Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 100%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_23.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phase.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_rvirus.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	585.5	97.6	133	Q9PWR7	Q9pwr7 rana catesb
2	554.5	92.4	133	Q98SM0	Q98sm0 rana catesb
3	483.5	80.6	132	Q98SM2	Q98sm2 rana catesb
4	474.5	79.1	133	Q98SL9	Q98sl9 rana catesb
5	467.5	77.9	133	Q98SL7	Q98sl7 rana catesb
6	444.5	74.1	132	Q98SM1	Q98sm1 rana catesb
7	372	62.0	132	Q9DF78	Q9df78 rana catesb
8	277.5	46.2	127	Q9I8V8	Q9i8v8 rana pipien
9	273.5	45.5	127	Q8UVX5	Q8uvx5 rana pipien
10	243	40.5	129	Q9DFY6	Q9dfy6 rana catesb
11	225.5	37.6	128	Q9DFY8	Q9dfy8 rana catesb
12	223.5	37.2	128	Q9DFY7	Q9dfy7 rana catesb
13	214.5	35.8	128	Q9DFY5	Q9dfy5 rana catesb
14	161	26.8	169	Q9W738	Q9w738 xenopus lae
15	128	21.3	170	Q9BEC1	Q9bec1 tragulus ja
16	121.5	20.2	116	Q9TVCO	Q9tvco sus scrofa

17	121.5	20.2	163	6	Q9BDC2	Q9bdc2 antilocapra
18	121	20.2	150	11	Q8VD94	Q8vd94 berylmys bo
19	119	19.8	150	11	Q8VD88	Q8vd88 rattus norv
20	118.5	19.8	144	6	Q9BH14	Q9bhl14 antilocapra
21	116.5	19.4	149	11	Q8K2T2	Q8k2t2 mus musculu
22	116.5	19.4	149	11	Q8CG63	Q8c6g3 mus musculu
23	116	19.3	150	11	Q8VD92	Q8vd92 rattus exul
24	113.5	18.9	152	11	Q8VD89	Q8vd89 rattus norv
25	113.5	18.8	119	6	Q9TV33	Q9tv33 bos taurus
26	111	18.5	148	11	Q8C663	Q8c663 mus musculu
27	110.5	18.4	124	6	Q9SNE6	Q9sne6 bubalus bub
28	109.5	18.2	148	11	Q8C7E4	Q8c7e4 mus musculu
29	109.5	18.2	149	11	Q8VD95	Q8vd95 berylmys bo
30	109	18.2	124	6	Q9BEC2	Q9bec2 tragulus ja
31	109	18.2	134	6	Q9BD89	Q9bdb9 tragulus ja
32	108.5	18.1	152	11	Q8VD84	Q8vdb4 rattus tiom
33	108.5	18.1	156	6	Q8SQ05	Q8sq05 leiothrix l
34	107.5	17.9	119	6	Q9TV28	Q9tv28 eulemur ful
35	107.5	17.9	119	6	Q9TV30	Q9tv30 saguinus oe
36	106.5	17.8	124	6	Q9TSF2	Q9tsf2 bos taurus
37	106.5	17.8	156	6	Q8SQ06	Q8sq06 ateles geof
38	105.5	17.6	142	6	Q9BEC3	Q9bec3 tragulus ja
39	105.5	17.6	156	6	Q8SQ08	Q8sq08 salmirl sci
40	105.5	17.6	156	6	Q8SQ07	Q8sq07 saguinus oe
41	104.5	17.4	152	11	Q8VD90	Q8vd90 rattus fusc
42	103.5	17.2	116	6	Q97933	Q97933 phocoenoide
43	103.5	17.2	149	11	Q8VD93	Q8vd93 rattus exul
44	102.5	17.1	116	6	Q97934	Q97934 pseudorca c
45	102.5	17.1	119	6	Q9TSQ6	Q9tsq6 cercopithec

ALIGNMENTS

RESULT 1

Q9PWR7 ID Q9PWR7 PRELIMINARY; PRT; 133 AA.
AC Q9PWR7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Ribonuclease precursor.
GN RCR.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP TISSUE=Liver;
RC MEDLINE=98165825; PubMed=9497170;
RX Huang H.C., Wang S.C., Leu Y.J., Lu S.C., Liao Y.D.;
RT "The Rana catesbeiana rcr gene encoding a cytotoxic ribonuclease.
RT Tissue distribution, cloning, purification, cytotoxicity, and active
RT residues for RNase activity.";
RL J. Biol. Chem. 273:6395-6401(1998).
DR EMBL; AF019104; AAD10702.1; --
DR HSP; P11916; IBC4.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnasea; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_Pc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
FT SIGNAL.
FT CHAIN 1 22 POTENTIAL.
SQ SEQUENCE 133 AA; 14762 MW; A7D62594F7D16FOC CRC64;
RIBONUCLEASE.
Query Match 97.6%; Score 585.5; DB 13; Length 133;
Best Local Similarity 97.3%; Pred. No. 4.3e-59;
Matches 108; Conservative 2; Mismatches 0; Indels 1; Gaps 1;
QY 1 QNWATFOQKHINTPII-CNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVINLV 59

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Db 23 QNWATFOQKHINTPII-NTILDNNIYVGGCKRVNTFISSATTVKAICTGVINLV 82
QY 60 LSTTRFQNLNCTRTSITPRPCPSYSSRTETNYICVKENQYPVHFAGIGRCP 110
Db 83 LSTTRFQNLNCTRTSITPRPCPSYSSRTETNYICVKENQYPVHFAGIGRCP 133

RESULT 2
Q98SM0
ID Q98SM0 PRELIMINARY; PRT; 133 AA.
AC Q98SM0;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE RNase A-type ribonuclease rc208 precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21539506; PubMed=11683320;
RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT "Rapid diversification of RNase A superfamily ribonuclease from the
RT bullfrog, Rana catesbeiana."
RL J. Mol. Evol. 53:31-38(2001).
DR EMBL; AF351209; AAK30255.1; -.
DR HSSP; P11916; 1BC4.
DR InterPro; IPR001427; RNaseA.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_PC; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL.
SQ SEQUENCE 133 AA; 14628 MW; 87FCF122C3499E02 CRC64;

Query Match 92.4%; Score 554.5; DB 13; Length 133;
Best Local Similarity 92.8%; Pred. No. 1.5e-55;
Matches 103; Conservative 2; Mismatches 5; Indels 1; Gaps 1;

QY 1 QNWATFOQKHINTPII-NTILDNNIYVGGCKRVNTFISSATTVKAICTGVINLV 59
Db 23 QNWATFOQKHINTPII-NTILDNNIYVGGCKRVNTFISSATTVKAICTGVINLV 82
QY 60 LSTTRFQNLNCTRTSITPRPCPSYSSRTETNYICVKENQYPVHFAGIGRCP 110
Db 83 LSTTRFQNLNCTRTSITPRPCPSYSSRTETNYICVKENQYPVHFAGIGRCP 133

RESULT 3
Q98SM2
ID Q98SM2 PRELIMINARY; PRT; 132 AA.
AC Q98SM2;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE RNase A-type ribonuclease rc203 precursor (RC-RNase7 precursor).
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21539506; PubMed=11683320;
RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT "Rapid diversification of RNase A superfamily ribonuclease from the
RT bullfrog, Rana catesbeiana."
RL J. Mol. Evol. 53:31-38(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
```

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RA Liao Y.-D., Tang P.-C., Jeng J.-T.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AF351207; AAK30253.1; -.
DR EMBL; AF359578; AAL87036.1; -.
DR HSSP; P11916; 1BC4.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnasea; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_PC; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL.
SQ SEQUENCE 132 AA; 14412 MW; 131A745187978687 CRC64;

Query Match 80.6%; Score 483.5; DB 13; Length 132;
Best Local Similarity 82.7%; Pred. No. 1.9e-47;
Matches 91; Conservative 6; Mismatches 12; Indels 1; Gaps 1;

QY 1 QNWATFOQKHINTPII-NTILDNNIYVGGCKRVNTFISSATTVKAICTGVINLV 59
Db 23 QNWATFOQKHINTPII-NTILDNNIYVGGCKRVNTFISSATTVKAICTGVINLV 82
QY 60 LSTTRFQNLNCTRTSITPRPCPSYSSRTETNYICVKENQYPVHFAGIGRCP 109
Db 83 LSTTRFQNLNCTRTSITPRPCPSYSSRTETNYICVKENQYPVHFAGIGRCP 132

RESULT 4
Q98SL9
ID Q98SL9 PRELIMINARY; PRT; 133 AA.
AC Q98SL9;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE RNase A-type ribonuclease rc212 precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21539506; PubMed=11683320;
RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT "Rapid diversification of RNase A superfamily ribonuclease from the
RT bullfrog, Rana catesbeiana."
RL J. Mol. Evol. 53:31-38(2001).
DR EMBL; AF351210; AAK30256.1; -.
DR HSSP; P11916; 1BC4.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnasea; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_PC; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL.
SQ SEQUENCE 133 AA; 14615 MW; C8785B236B2B5E4E CRC64;

Query Match 79.1%; Score 474.5; DB 13; Length 133;
Best Local Similarity 77.5%; Pred. No. 2e-46;
Matches 86; Conservative 12; Mismatches 12; Indels 1; Gaps 1;

QY 1 QNWATFOQKHINTPII-NTILDNNIYVGGCKRVNTFISSATTVKAICTGVINLV 59
Db 23 QNWATFOQKHINTPII-NTILDNNIYVGGCKRVNTFISSATTVKAICTGVINLV 82
QY 60 LSTTRFQNLNCTRTSITPRPCPSYSSRTETNYICVKENQYPVHFAGIGRCP 110
Db 83 LSTTRFQNLNCTRTSITPRPCPSYSSRTETNYICVKENQYPVHFAGIGRCP 133

RESULT 5
Q98SL8
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ID Q98SL8 PRELIMINARY; PRT; 133 AA.
AC Q98SL8;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Rnase A-type ribonuclease rc218 precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21539506; PubMed=11683320;
RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT "Rapid diversification of Rnase A superfamily ribonuclease from the
RL bullfrog, Rana catesbeiana."
DR EMBL; AF351211; AA30257.1; -.
DR HSSP; P11916; 1BC4.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL.
SQ SEQUENCE 133 AA; 14590 MW; 8B40B9A94FASB943 CRC64;

Query Match 77.9%; Score 467.5; DB 13; Length 133;
Best Local Similarity 75.7%; Pred. No. 1.3e-45;
Matches 84; Conservative 14; Mismatches 12; Indels 1; Gaps 1;

QY 1 QNWATFOQKHINTPII-CNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVINLV 59
Db 23 QNWATFOEQHITSSINCNSIMNNSLYVGGQCKVNTFIASSATTVKICSGVTDKV 82
QY 60 LSTTRFOLNCTRTSITPRPCPYSSRTETNYICVKCENQYVPHFAGIGRCP 110
Db 83 LSSTKFOLDICTRIFITPRPCPYSSRTETNYICVKCENQYVPHFAGIGQCP 133

RESULT 6
Q98SM1 PRELIMINARY; PRT; 132 AA.
ID Q98SM1;
AC Q98SM1;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Rnase A-type ribonuclease rc204 precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21539506; PubMed=11683320;
RA Rosenberg H.F., Zhang J., Liao Y.-D., Dyer K.D.;
RT "Rapid diversification of Rnase A superfamily ribonuclease from the
RL bullfrog, Rana catesbeiana."
DR EMBL; AF351208; AA30254.1; -.
DR HSSP; P11916; 1BC4.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL.
SQ SEQUENCE 132 AA; 14704 MW; 95D61760F729868E CRC64;

Query Match 74.1%; Score 444.5; DB 13; Length 132;
Best Local Similarity 77.3%; Pred. No. 5.4e-43;

Matches 85; Conservative 8; Mismatches 16; Indels 1; Gaps 1;

QY 1 QNWATFOQKHINTPII-CNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVINLV 59
Db 23 QDMPTFOQKHIPSTSSIDCNTIMDKOIYVRGCKKVNFTFIYATTVKAICTGVLSNV 82
QY 60 LSTTRFOLNCTRTSITPRPCPYSSRTETNYICVKCENQYVPHFAGIGRC 109
Db 83 LSTTRFOLXXXTRFITRSPCPYSSRTETNKICVKCENYVPHFAGIGKC 132

RESULT 7
Q9DF78 PRELIMINARY; PRT; 132 AA.
ID Q9DF78;
AC Q9DF78;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE RC-RNaseL1 ribonuclease precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Liver;
RX MEDLINE=20512555; PubMed=11058105;
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RT "Purification and cloning of cytotoxic ribonucleases from Rana
RL catesbeiana (bullfrog).";
RL Nucleic Acids Res. 28:4097-4104(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF288642; AAG30414.2; -.
DR HSSP; P11916; 1BC4.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal.
FT SIGNAL.
FT CHAIN 1 21 POTENTIAL.
FT CHAIN 22 132 RC-RNASEL1 RIBONUCLEASE.
SQ SEQUENCE 132 AA; 14625 MW; D8D9A517452FBES3 CRC64;

Query Match 62.0%; Score 372; DB 13; Length 132;
Best Local Similarity 64.9%; Pred. No. 1e-34;
Matches 72; Conservative 10; Mismatches 27; Indels 2; Gaps 2;

QY 1 QNWATFOQKHINTPII-CNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVI 58
Db 22 QNNAKFKKHITSSIDCNTIMDKAIYVGGCKERNFTFISSDNVKAICSGVSPDK 81
QY 59 VLSTTRFOLNCTRTSITPRPCPYSSRTETNYICVKCENQYVPHFAGIGRC 109
Db 82 ELSTTSFKLNTICRDSITPRPCPYHSPDNKNKICVKCEKQLPVHFVGIGKC 132

RESULT 8
Q918V8 PRELIMINARY; PRT; 127 AA.
ID Q918V8;
AC Q918V8;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Onconase variant rapLr1 precursor
OS Rana pipiens (Northern leopard frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8404;
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RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF242553; AAG31439.1; -.
DR HSSP: P22069; 10NC.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; rnaaseA; 1.
DR ProDom: PD000535; RNaseA; 1.
DR PROSITE: PS00127; RNASE_PANCREATIC; 1.
KW SIGNAL.
FT SIGNAL.
FT CHAIN.
SQ SEQUENCE 128 AA; 14839 MW; 989719CF52053ECC CRC64;

Query Match 37.6%; Score 225.5; DB 13; Length 128;
Best Local Similarity 39.3%; Pred. No. 5.3e-18;
Matches 44; Conservative 21; Mismatches 38; Indels 9; Gaps 4;

Qy 1 QNWATFOQKHINT-PIICNTILDNNIYVGGQCKRVNTFISSATTVKAICTGV-INLN 58
Db 24 QNWTFQKGLTDRVCKDAEMKKALF----DCKQNTFIYARPGRVQALCKNIIVSKN 79

Qy 59 VLSTTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRCP 110
Db 80 VLSTDEFYLCNRIKL---PCHYKLKSSNTICITCKENKLPVHFVAVEECP 128

RESULT 12
Q9DFV7
ID Q9DFY7 PRELIMINARY; PRT; 128 AA.
AC Q9DFY7;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE RC-RNase3 ribonuclease precursor.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
NCBI_TaxID=8400;
RN [1]
RC TISSUE=Liver;
RX MEDLINE=20512555; PubMed=11058105;
Liao Y.-D., Huang H.-C., Leu Y.-J., Wei C.-W., Tang P.-C., Wang S.-C.;
" Purification and cloning of cytotoxic ribonucleases from Rana
catesbeiana (bullfrog).";
Nucleic Acids Res. 28:4097-4104(2000).
FT SIGNAL.
FT CHAIN.
SQ SEQUENCE 128 AA; 14839 MW; 989719CF52053ECC CRC64;

Query Match 35.8%; Score 214.5; DB 13; Length 128;
Best Local Similarity 38.4%; Pred. No. 9.6e-17;
Matches 43; Conservative 20; Mismatches 40; Indels 9; Gaps 4;

C/ 1 QNWATFOQKHINT-PIICNTILDNNIYVGGQCKRVNTFISSATTVKAICTGV-INLN 58
Db 24 QNWTFQKGLTDRVCKDAEMKKALF----DCKQNTFIYARPGRVQALCKNIIVSKN 79

Qy 59 VLSTTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRCP 110
Db 80 VLSTDEFYLCNRIKL---PCHYKLKSSNTICITCKENKLPVHFVAVEECP 128

RESULT 14
Q9W738
ID Q9W738 PRELIMINARY; PRT; 169 AA.
AC Q9W738;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE FRL2 protein.
GN FRL2.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
NCBI_TaxID=8355;
RN [1]
RC TISSUE=Liver;
RX MEDLINE=96069863; PubMed=7585965;
Kinoshita N., Minshull J., Kirschner M.W.;
"The identification of two novel ligands of the FGF receptor by a
yeast screening method and their activity in Xenopus development.";
Cell 83:621-630(1995).
FT SIGNAL.
FT CHAIN.
SQ SEQUENCE FROM N.A.
Kinoshita N., Kirschner M.W.;
Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF159166; AAD41901.1; -.
DR HSSP: P00656; 1LSQ.
DR InterPro: IPR001427; RNaseA.

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OM protein - protein search, using sw model

Run on: January 22, 2004, 12:01:20 ; Search time 34.9213 Seconds
(without alignment)
504.524 Million cell updates/sec

Title: US-09-622-613C-17

Perfect score: 607

Sequence: 1 MQNWATPQKHIIPTIICN.....ICVKCENQYVHFAGIGRCF 111

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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- 2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
- 3: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
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- 19: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
- 20: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
- 21: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
- 22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
- 23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
- 24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	607	100.0	111	20	AAV28873
2	602	99.2	110	20	AAV28872
3	602	99.2	111	20	AAV28878
4	601	99.0	111	20	AAV28876
5	597	98.4	110	20	AAV28877
6	596	98.2	110	20	AAV28874
7	588.5	97.0	111	20	AAV33321
8	286.5	47.2	105	20	AAV28867
9	284.5	46.9	104	18	AAW06544

10	283.5	46.7	105	20	AAV28869	Recombinant Met (-1
11	282.5	46.5	105	20	AAV39400	Recombinant frog O
12	281.5	46.4	104	20	AAV28865	Rana pipiens liver
13	281.5	46.4	105	20	AAV28871	Recombinant Met (-1
14	281.5	46.4	127	20	AAV28879	Rana pipiens Clone
15	279.5	46.0	105	18	AAV35123	R. pipiens recombi
16	279.5	46.0	355	18	AAV35125	R. pipiens recombi
17	279.5	46.0	358	18	AAV35130	R. pipiens recombi
18	278.5	45.9	104	20	AAV28866	Recombinant RAPUR1
19	277.5	45.7	104	18	AAW30301	Recombinant onc pr
20	277.5	45.7	104	22	AAW31666	Amino acid sequenc
21	277.5	45.7	104	23	ABG32650	Northern leopard f
22	277.5	45.7	112	18	AAW35118	R. pipiens recombi
23	277.5	45.7	251	18	AAW35134	R. pipiens recombi
24	277.5	45.7	254	18	AAW35135	R. pipiens recombi
25	277.5	45.7	355	18	AAW35139	R. pipiens recombi
26	277.5	45.7	355	18	AAW35133	R. pipiens recombi
27	277.5	45.7	366	18	AAW35132	R. pipiens recombi
28	277.5	45.7	379	18	AAW35126	R. pipiens recombi
29	276.5	45.6	104	20	AAV28870	Recombinant RAPUR1
30	274.5	45.2	104	12	AAW12344	Protein with activ
31	274.5	45.2	104	15	AAW47303	ONCONASE (pharmac
32	274.5	45.2	104	17	AAW00736	Protein derived fr
33	274.5	45.2	104	18	AAW06543	Antitumour protein
34	274.5	45.2	104	18	AAW14065	Oncogene (RTM) pro
35	274.5	45.2	104	20	AAV33322	Frog onconase prot
36	274.5	45.2	104	20	AAW88233	Rana pipiens RNase
37	272.5	44.9	104	22	AAW31667	Amino acid sequenc
38	272.5	44.9	104	23	ABG31617	Northern leopard f
39	272.5	44.9	105	18	AAW35116	R. pipiens recombi
40	272.5	44.9	106	18	AAW35122	R. pipiens recombi
41	272.5	44.9	107	18	AAW35117	R. pipiens recombi
42	271.5	44.7	104	18	AAW30302	Recombinant onc pr
43	271.5	44.7	105	18	AAW35115	R. pipiens recombi
44	268.5	44.2	358	18	AAW35127	R. pipiens recombi
45	268.5	44.2	365	18	AAW35131	R. pipiens recombi

ALIGNMENTS

RESULT 1

AAV28873

ID AAV28873 standard; Protein; 111 AA.

XX

AC AAV28873;

XX

DT 25-JAN-2000 (first entry)

XX

DE Recombinant Met (-1) RaCOR1.

XX

KW Recombinant Met (-1) Rana catesbeiana oocyte ribonuclease; RaCOR1; CD22;
covalently bound; LL2 antibody; ligand binding moiety; cancerous B cell;
Kaposi's sarcoma; human chorionic gonadotropin; hCG; signal peptide;
KW recombinant ribonuclease; cytotoxic fusion protein; cancer; bullfrog;
KW RNase; autoimmune disease.

OS

OS Rana catesbeiana.

OS

XX

PH Key Location/Qualifiers

FT Misc-difference 1 /note= "Met not found in wild type RaCOR1"

XX

XX WO9950398-A2.

PN

XX

PD 07-OCT-1999.

XX

XX 26-MAR-1999; 99WO-US06641.

XX

XX 27-MAR-1998; 98US-0079751.

XX

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX PI Newton DL, Rybak SM;
 XX DR WPI; 1999-610847/52.
 XX DR N-PSDB; AAZ08131.
 XX PT New recombinant ribonucleases, used for killing target cells, e.g. for
 PT treating cancers, viral infections or autoimmune diseases -
 XX PS Claim 22; Page 63; 71pp; English.
 XX CC The present sequence is a recombinant Rana catesbeiana oocyte
 CC ribonuclease (RaCOR1) protein with Met at position 1. Carboxy terminal
 CC end of recombinant RaCOR1 has a covalently bound ligand binding moiety,
 CC which can be a LL2 antibody directed against CD22 on cancerous B cells or
 CC human chorionic gonadotrophin (hCG) effective against Kaposi's sarcoma
 CC cells. Recombinant ribonucleases can be expressed in bacteria without an
 CC C-terminal methionine due to the presence of a signal peptide that is
 CC cleaved by bacteria. The soluble expression of ribonuclease allows the
 CC proteins to be fused in-frame with ligand binding moieties to form
 CC cytotoxic fusion proteins. They can be used for treatment of cancer and
 CC autoimmune diseases.
 XX SQ Sequence 111 AA;
 Query Match 100.0%; Score 607; DB 20; Length 111;
 Best Local Similarity 100.0%; Pred. No. 7.2e-62; Indels 0; Gaps 0;
 Matches 111; Conservative 0; Mismatches 0;
 QY 1 MNWATFOQKHIIPTIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINMNV 60
 DB 1 MNWATFOQKHIIPTIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINMNV 60
 QY 61 LSTTRFQLNCTRTSITPRPCPSYSSRTETNYICVKCENQYPVHFAGIGRCP 111
 DB 61 LSTTRFQLNCTRTSITPRPCPSYSSRTETNYICVKCENQYPVHFAGIGRCP 111
 RESULT 2
 AAY28872
 ID AAY28872 standard; Protein; 110 AA.
 XX AC AAY28872;
 XX DT 25-JAN-2000 (first entry)
 XX DE Rana catesbeiana oocyte ribonuclease (RaCOR1) amino acid sequence.
 XX KW Rana catesbeiana oocyte ribonuclease; RaCOR1; covalently bound; CD22;
 KW LL2 antibody; ligand binding moiety; cancerous B cell; Kaposi's Sarcoma;
 KW human chorionic gonadotrophin; hCG; recombinant ribonuclease; bullfrog;
 KW signal peptide; cytotoxic fusion protein; cancer; autoimmune disease;
 KW RNase.
 XX OS Rana catesbeiana.
 XX OS Synthetic.
 XX PN WO9950398-A2.
 XX PD 07-OCT-1999.
 XX PF 26-MAR-1999; 99WO-US06641.
 XX PR 27-MAR-1998; 98US-0079751.
 XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX PI Newton DL, Rybak SM;
 XX DR WPI; 1999-610847/52.
 XX DR N-PSDB; AAZ08130.
 XX PT New recombinant ribonucleases, used for killing target cells, e.g. for

PT treating cancers, viral infections or autoimmune diseases -
 XX PS Claim 22; Page 62; 71pp; English.
 XX CC The present sequence is a Rana catesbeiana oocyte ribonuclease (RaCOR1)
 CC protein encoded by a cDNA modified for expression in E. coli. Carboxy
 CC terminal end of RaCOR1 has a covalently bound ligand binding moiety,
 CC which can be a LL2 antibody directed against CD22 on cancerous B cells
 CC or human chorionic gonadotrophin (hCG) effective against Kaposi's
 CC Sarcoma cells. Recombinant ribonucleases can be expressed in bacteria
 CC without an N-terminal methionine due to the presence of a signal peptide
 CC that is cleaved by bacteria. The soluble expression of ribonuclease
 CC allows the proteins to be fused in-frame with ligand binding moieties to
 CC form cytotoxic fusion proteins. They can be used for treatment of cancer
 CC and autoimmune diseases.
 XX SQ Sequence 110 AA;
 Query Match 99.2%; Score 602; DB 20; Length 110;
 Best Local Similarity 100.0%; Pred. No. 2.7e-61;
 Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 QNWATFOQKHIIPTIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINMNV 61
 DB 1 QNWATFOQKHIIPTIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINMNV 60
 QY 62 STTRFQLNCTRTSITPRPCPSYSSRTETNYICVKCENQYPVHFAGIGRCP 111
 DB 61 STTRFQLNCTRTSITPRPCPSYSSRTETNYICVKCENQYPVHFAGIGRCP 110
 RESULT 3
 AAY28878
 ID AAY28878 standard; Protein; 111 AA.
 XX AC AAY28878;
 XX DT 25-JAN-2000 (first entry)
 XX DE Recombinant Met (-1) RaCOR1 Gln1Ser amino acid sequence.
 XX KW Recombinant Met (-1) Rana catesbeiana oocyte ribonuclease Gln1Ser; RaCOR1;
 KW covalently bound; LL2 antibody; ligand binding moiety; cancerous B cell;
 KW Kaposi's sarcoma; human chorionic gonadotrophin; hCG; signal peptide;
 KW recombinant ribonuclease; cytotoxic fusion protein; cancer; bullfrog;
 KW CD22; RNase; autoimmune disease.
 XX OS Rana catesbeiana.
 XX OS Synthetic.
 XX FH Key Location/Qualifiers
 FT Misc-difference 1 /note= "Met not found in wild type RaCOR1"
 FT Misc-difference 2 /note= "Wild type Gln replaced with Ser"
 XX PN WO9950398-A2.
 XX PD 07-OCT-1999.
 XX PF 26-MAR-1999; 99WO-US06641.
 XX PR 27-MAR-1998; 98US-0079751.
 XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX PI Newton DL, Rybak SM;
 XX DR WPI; 1999-610847/52.
 XX DR N-PSDB; AAZ08135.
 XX PT New recombinant ribonucleases, used for killing target cells, e.g. for
 PT treating cancers, viral infections or autoimmune diseases -

XX PS Claim 22; Page 68; 71pp; English.

XX CC The present sequence is a recombinant Rana catesbeiana ribonuclease

CC (RaCOR1) protein with Met at position 1 and Gln28Ser. Carboxy terminal end

CC of recombinant RaCOR1 has a covalently bound ligand binding moiety, which

CC can be a LL2 antibody directed against CD22 on cancerous B cells or human

CC chorionic gonadotrophin (hCG) effective against Kaposi's sarcoma cells.

CC Recombinant ribonucleases can be expressed in bacteria without an N-

CC terminal methionine due to the presence of a signal peptide that is

CC cleaved by bacteria. The soluble expression of ribonuclease allows the

CC proteins to be fused in-frame with ligand binding moieties to form

CC cytotoxic fusion proteins. They can be used for treatment of cancer and

CC autoimmune diseases.

XX SQ Sequence 111 AA;

Query Match 99.2%; Score 602; DB 20; Length 111;

Best Local Similarity 99.1%; Pred. No. 2.7e-61;

Matches 110; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MOWATFOQKHINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINNV 60

DB 1 MSNWATFOQKHINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINNV 60

QY 61 LSTTRFQNLCTRTSITPRPCPYSSRTETNYICVKCENQYPVHPAGIGRCP 111

DB 61 LSTTRFQNLCTRTSITPRPCPYSSRTETNYICVKCENQYPVHPAGIGRCP 111

RESULT 4

AAV28876

ID AAY28876 standard; Protein; 111 AA.

XX AC AAY28876;

XX DT 25-JAN-2000 (first entry)

XX DE Recombinant Met(-1) RaCOR1 Met22Leu Met57Leu-(His)6 protein.

XX KW Met(-1) Rana catesbeiana ribonuclease Met22Leu Met57Leu-(His)6; RaCOR1;

XX KW recombinant; CD22; covalently bound; LL2 antibody; ligand binding moiety;

XX KW cancerous B cell; Kaposi's sarcoma; human chorionic gonadotrophin; hCG;

XX KW signal peptide; recombinant ribonuclease; cytotoxic fusion protein;

XX KW cancer; bullfrog; RNase; autoimmune disease.

XX OS Rana catesbeiana.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT Misc-difference 1 /note= "(His)6 histidine tag attached to N-terminal Met"

FT Misc-difference 1 /note= "Met not found in wild type RaCOR1"

FT Misc-difference 23 /note= "Wild type Met replaced with Leu"

FT Misc-difference 58 /note= "Wild type Met replaced with Leu"

XX PN W09950398-A2.

XX PD 07-OCT-1999.

XX PF 26-MAR-1999; 99WO-US06641.

XX PR 27-MAR-1998; 98US-0079751.

XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX PI Newton DL, Rybak SM;

XX DR WPI: 1999-610847/52.

XX DR N-PSDB; AA208133.

XX PT New recombinant ribonucleases, used for killing target cells, e.g. for

PT treating cancers, viral infections or autoimmune diseases -

XX PS Claim 22; Page 66; 71pp; English.

XX CC The present sequence is a recombinant Rana catesbeiana oocyte

CC ribonuclease (RaCOR1) protein with Met at position 1 attached to a

CC (His)6 tag, Met23Leu and Met58Leu. Carboxy terminal end of recombinant

CC RaCOR1 has a covalently bound ligand binding moiety, which can be a LL2

CC antibody directed against CD22 on cancerous B cells or human chorionic

CC gonadotrophin (hCG) effective against Kaposi's sarcoma cells. Recombinant

CC ribonucleases can be expressed in bacteria without an N-terminal

CC methionine due to the presence of a signal peptide that is cleaved by

CC bacteria. The soluble expression of ribonuclease allows the proteins to

CC be fused in-frame with ligand binding moieties to form cytotoxic fusion

CC proteins. They can be used for treatment of cancer and autoimmune

CC diseases.

XX SQ Sequence 111 AA;

Query Match 99.0%; Score 601; DB 20; Length 111;

Best Local Similarity 98.2%; Pred. No. 3.5e-61;

Matches 109; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOWATFOQKHINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINNV 60

DB 1 MOWATFOQKHINTPIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVINNV 60

QY 61 LSTTRFQNLCTRTSITPRPCPYSSRTETNYICVKCENQYPVHPAGIGRCP 111

DB 61 LSTTRFQNLCTRTSITPRPCPYSSRTETNYICVKCENQYPVHPAGIGRCP 111

RESULT 5

AAV28877

ID AAY28877 standard; Protein; 110 AA.

XX AC AAY28877;

XX DT 25-JAN-2000 (first entry)

XX DE Recombinant RaCOR1 Gln1Ser amino acid sequence.

XX KW Recombinant Rana catesbeiana oocyte ribonuclease; RaCOR1 Gln1Ser; CD22;

XX KW covalently bound; LL2 antibody; ligand binding moiety; cancerous B cell;

XX KW bullfrog; Kaposi's sarcoma; human chorionic gonadotrophin; hCG; RNase;

XX KW signal peptide; recombinant ribonuclease; cytotoxic fusion protein;

XX KW cancer; autoimmune disease.

XX OS Rana catesbeiana.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT Misc-difference 1 /note= "Wild type Gln replaced with Ser"

XX PN W09950398-A2.

XX PD 07-OCT-1999.

XX PF 26-MAR-1999; 99WO-US06641.

XX PR 27-MAR-1998; 98US-0079751.

XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX PI Newton DL, Rybak SM;

XX DR WPI: 1999-610847/52.

XX DR N-PSDB; AA208134.

XX PT New recombinant ribonucleases, used for killing target cells, e.g. for

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PT treating cancers, viral infections or autoimmune diseases -
XX Claim 22; Page 67; 71pp; English.
XX
CC The present sequence is a recombinant Rana catesbeiana oocyte
CC ribonuclease (RaCOR1) protein with Gln1Ser. Carboxy terminal end of
CC recombinant RaCOR1 has a covalently bound ligand binding moiety, which
CC can be a LL2 antibody directed against CD22 on cancerous B cells or
CC human chorionic gonadotrophin (hCG) effective against Kaposi's sarcoma
CC cells. Recombinant ribonucleases can be expressed in bacteria without an
CC N-terminal methionine due to the presence of a signal peptide that is
CC cleaved by bacteria. The soluble expression of ribonuclease allows the
CC proteins to be fused in-frame with ligand binding moieties to form
CC cytotoxic fusion proteins. They can be used for treatment of cancer and
CC autoimmune diseases.
XX
SQ Sequence 110 AA;
Query Match 98.4%; Score 597; DB 20; Length 110;
Best Local Similarity 100.0%; Pred. No. 1e-60;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 3 NWATFOQKHIIINTPIICNTIMDNIIYVGGQCKRVNTFISSATTVKAICTGVINMNVLS 62
Db 2 NWATFOQKHIIINTPIICNTIMDNIIYVGGQCKRVNTFISSATTVKAICTGVINMNVLS 61
Qy 63 TTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
Db 62 TTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
RESULT 6
AA28874
ID AAY28874 standard; Protein; 110 AA.
XX
AC AAY28874;
XX
DT 25-JAN-2000 (first entry)
XX
DE Recombinant RaCOR1 Met22Leu Met57Leu amino acid sequence.
XX
KW Recombinant Rana catesbeiana oocyte ribonuclease; covalently bound;
KW RaCOR1 Met22Leu Met57Leu; LL2 antibody; ligand binding moiety; CD22;
KW cancerous B cell; Kaposi's sarcoma; human chorionic gonadotrophin; hCG;
KW signal peptide; recombinant ribonuclease; cytotoxic fusion protein;
KW cancer; bullfrog; RNase; autoimmune disease.
XX
OS Rana catesbeiana.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 22 /note= "Wild type Met replaced with Leu"
FT Misc-difference 57 /note= "Wild type Met replaced with Leu"
XX
PN WO9950398-A2.
XX
PD 07-OCT-1999.
XX
PF 26-MAR-1999; 99WO-US06641.
XX
PR 27-MAR-1998; 98US-0079751.
XX
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Newton DL, Rybak SM;
XX
DR WPI; 1999-610847/52.
DR N-PSDB; AAZ08132.
XX
PT New recombinant ribonucleases, used for killing target cells, e.g. for
treating cancers, viral infections or autoimmune diseases -

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XX Claim 22; Page 64; 71pp; English.
XX
CC The present sequence is a recombinant Rana catesbeiana oocyte
CC ribonuclease (RaCOR1) protein with Met22Leu Met57Leu. Carboxy terminal
CC end of recombinant RaCOR1 has a covalently bound ligand binding moiety,
CC which can be a LL2 antibody directed against CD22 on cancerous B cells
CC or human chorionic gonadotrophin (hCG) effective against Kaposi's sarcoma
CC cells. Recombinant ribonucleases can be expressed in bacteria without an
CC N-terminal methionine due to the presence of a signal peptide that is
CC cleaved by bacteria. The soluble expression of ribonuclease allows the
CC proteins to be fused in-frame with ligand binding moieties to form
CC cytotoxic fusion proteins. They can be used for treatment of cancer and
CC autoimmune diseases.
XX
SQ Sequence 110 AA;
Query Match 98.2%; Score 596; DB 20; Length 110;
Best Local Similarity 98.2%; Pred. No. 1.3e-60;
Matches 108; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 2 QNWATFOQKHIIINTPIICNTIMDNIIYVGGQCKRVNTFISSATTVKAICTGVINMNVL 61
Db 1 QNWATFOQKHIIINTPIICNTILDNNIIYVGGQCKRVNTFISSATTVKAICTGVINLNL 60
Qy 62 STTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
Db 61 STTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
RESULT 7
AA28874
ID AAY33321 standard; Protein; 111 AA.
XX
AC AAY33321;
XX
DT 29-NOV-1999 (first entry)
XX
DE Frog lectin protein fragment.
XX
KW Cytotoxic; RNase; ribonuclease; pancreatic; antibody; light chain;
KW heavy chain; cell surface marker; treatment; tumor; viral infection;
KW parasite infection; immune dysfunctional cell; autoimmune disease;
KW contraceptive; cell separation; transplantation; bone marrow ablation;
KW leukemia cell; T-cell; graft-versus-host disease; bullfrog; lectin.
XX
OS Rana catesbeiana.
XX
PN US955073-A.
XX
PD 21-SEP-1999.
XX
PF 09-JUL-1997; 97US-0801848.
XX
PR 22-SEP-1993; 93US-0125462.
PR 22-OCT-1991; 91US-0779195.
PR 20-APR-1990; 90US-0510696.
PR 04-FEB-1993; 93US-0014082.
XX
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Rybak SM, Newton DL, Nicholls PJ, Youle RJ;
XX
DR WPI; 1999-560488/47.
XX
PT Recombinantly fused pancreatic RNase-targeting proteins useful for
treating tumors, infections, immune or autoimmune disorders and as a
contraceptive -
XX
PS Example 3; Fig 19; 47pp; English.
XX
PT This invention describes a novel nucleic acid construct comprising
sequences encoding functional pancreatic RNase and a second protein

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CC (preferably the light and heavy chains of an antibody) which binds a
 CC specific cell surface marker on a target cell and functions as a
 CC cytotoxic agent. The products can be used for selectively killing cells
 CC expressing a specific surface marker. They can be used for treating
 CC tumors or infected cells (e.g. cells infected by viruses (especially
 CC latent or chronic virus infections, such as human immunodeficiency virus
 CC (HIV)-1, Epstein-Barr virus, herpes viruses (herpes simplex types I and
 CC II), hepatitis viruses (B, non-A-non-B, and delta), herpes zoster,
 CC cytomegalovirus) and cells infected with parasites (such as the malaria
 CC parasite)). They can also be used for treating immune dysfunctional cells
 CC in immune and autoimmune diseases. Additionally, they may be used as
 CC contraceptives. Finally they can also be used for cell separation in
 CC vitro by selectively killing unwanted types of cells (e.g. in bone
 CC marrow) prior to transplantation into a patient undergoing marrow
 CC ablation by radiation or for killing leukemia cells or T-cells that would
 CC cause graft-versus-host disease. This sequence represents a bullfrog
 CC (Rana catesbeiana) lectin used to describe the method of the invention.

XX Sequence 111 AA;
 SQ Query Match 97.0%; Score 588.5; DB 20; Length 111;
 Best Local Similarity 98.2%; Pred. No. 9.7e-60;
 Matches 109; Conservative 1; Mismatches 0; Indels 1; Gaps 1;
 QY 2 QNWTATFOOKHIIINTPII-CNTIMDNNIYVGGQCKRVNTFIISATTVKAICTGVINNV 60
 Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 1 ENWTATFOOKHIIINTPIINCNTIMDNNIYVGGQCKRVNTFIISATTVKAICTGVINNV 60
 QY 61 LSTTRFOLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
 Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 61 LSTTRFOLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111

RESULT 8
 AAY28867
 ID AAY28867 standard; Protein; 105 AA.
 XX
 AC AAY28867;
 XX
 DT 25-JAN-2000 (first entry)
 XX
 DE Recombinant Met (-1) RaPLR1.
 XX
 KW Recombinant Met (-1) Rana pipiens ribonuclease; RaPLR1; CD22; RNase;
 KW covalently bound; L2 antibody; ligand binding moiety; cancerous B cell;
 KW Kaposi's sarcoma; human chorionic gonadotropin; hCG; signal peptide;
 KW recombinant ribonuclease; cytotoxic fusion protein; cancer; frog;
 KW autoimmune disease.
 XX
 OS Rana pipiens.
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 XX Misc-difference 1 /note= "Met not found in wild type RaPLR1"
 FT
 FT
 FT
 XX WO9950398-A2.
 XX
 XX 07-OCT-1999.
 XX
 XX 26-MAR-1999; 99WO-US06641.
 XX
 XX 27-MAR-1998; 98US-0079751.
 XX
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PA
 XX Newton DL, Rybak SM;
 PI
 XX WPI; 1999-610847/52.
 XX N-PSDB; AA208126.
 DR
 XX New recombinant ribonucleases, used for killing target cells, e.g. for
 PT treating cancers, viral infections or autoimmune diseases

XX Claim 34; Page 57; 71pp; English.
 PS
 XX The present sequence is a recombinant Rana pipiens ribonuclease (RaPLR1)
 CC protein with Met at position 1. Carboxy terminal end of recombinant
 CC RaPLR1 has a covalently bound ligand binding moiety, which can be a L2
 CC antibody directed against CD22 on cancerous B cells or human chorionic
 CC gonadotropin (hCG) effective against Kaposi's sarcoma cells. Recombinant
 CC ribonucleases can be expressed in bacteria without an N-terminal
 CC methionine due to the presence of a signal peptide that is cleaved by
 CC bacteria. The soluble expression of ribonuclease allows the proteins to
 CC be fused in-frame with ligand binding moieties to form cytotoxic fusion
 CC proteins. They can be used for treatment of cancer and autoimmune
 CC diseases.
 XX
 SQ Sequence 105 AA;
 Query Match 47.2%; Score 286.5; DB 20; Length 105;
 Best Local Similarity 50.0%; Pred. No. 4.4e-25;
 Matches 56; Conservative 15; Mismatches 32; Indels 9; Gaps 4;
 QY 1 MQNWTATFOOKHIIINT-PIICNTIMDNNIYVGGQCKRVNTFIISATTVKAICTGVI-NM 58
 Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 1 MODWLTTFQKHILTRDVCNNIMSTNLF----HCKDKNTFIYSRPEVKAICKGIIASK 56
 QY 59 NVLSTTRFOLNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
 Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 57 NVLTSEFYLSDC---NVTSPCKYKLUKSTNTFCVTCTENQAPVHFVGVGHC 105

RESULT 9
 AAW06544
 ID AAW06544 standard; protein; 104 AA.
 XX
 AC AAW06544;
 XX
 DT 22-AUG-1997 (first entry)
 XX
 DE Antitumour protein from Rana pipiens oocytes.
 XX
 KW Tumour; chemotherapy; radiotherapy; frog.
 XX
 OS Rana pipiens.
 XX
 XX WO9639428-A1.
 XX
 XX 12-DEC-1996.
 XX
 XX 03-JUN-1996; 96WO-US08304.
 XX
 XX 06-JUN-1995; 95US-0467955.
 XX
 XX (ALFA-) ALFACELL CORP.
 XX
 XX Ardelt WJ;
 XX
 XX WPI; 1997-043063/04.
 XX
 XX Antitumour proteins from Rana pipiens oocyte(s) - have fewer
 XX disadvantages than chemotherapy, surgery and radiotherapy
 XX
 XX Claim 8; Page 28; 45pp; English.
 XX
 XX The present sequence is a specifically claimed example of an
 CC antitumour protein from the generic protein in AAW18224, with the
 CC molecular weight 12000. This is one of two preferred proteins (the
 CC other in AAW06543) that have been isolated from Rana pipiens oocytes.
 CC Both proteins have a blocked amino terminal group and are essentially
 CC free of carbohydrates. The proteins are used to treat tumours. Use of
 CC the peptides has fewer disadvantages than chemotherapy, radiotherapy
 CC and surgery in the treatment of tumours.
 XX
 XX Sequence 104 AA;
 SQ

Query Match		46.9%;	Score 284.5;	DB 18;	Length 104;
Best Local Similarity		49.5%;	Pred. No. 7.4e-25;		
Matches		55;	Conservative 16;	Mismatches 31;	Indels 9; Gaps 4;
QY	2	QNWATFOQKHINT-PIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVI-NMN	59		
DB	1	EDMLTFQKHGVTNRDVCNNIMSTNLF-...HCKDKNTFIYSRPEPVKAICKGIIASKN	56		
QY	60	VLSSTRFQNLCTRTSITPRPCPYSSRTETNYICVKCENQYVHPFAGIGRC	110		
DB	57	VLTTFSEFVSLDC---NVTSPCKYKLLKSTNKFVTCENQAPVHPFVGVRG	104		
RESULT 10					
AAV28869					
ID	AAV28869	standard; Protein; 105 AA.			
XX	AC	AAV28869;			
XX	DT	25-JAN-2000 (first entry)			
XX	DE	Recombinant Met (-1) RaPLR1 Met23Leu- (His)6 protein.			
XX	KW	Recombinant Met (-1) Rana pipiens ribonuclease Met23Leu- (His)6; RaPLR1;			
KW	CD22; covalently bound; LL2 antibody; ligand binding moiety; RNase;				
KW	cancerous B cell; Kaposi's sarcoma; human chorionic gonadotrophin; hCG;				
KW	signal peptide; recombinant ribonuclease; cytotoxic fusion protein;				
KW	cancer; frog; autoimmune disease.				
XX	Rana pipiens.				
OS	Synthetic.				
XX	Key	Location/Qualifiers			
FH	Misc-difference 1	/note= "(His)6 histidine tag attached to N-terminal Met"			
FT	Misc-difference 1	/note= "Met not found in wild type RaPLR1"			
FT	Misc-difference 24	/note= "Wild type Met replaced with Leu"			
XX	WO9950398-A2.				
XX	07-OCT-1999.				
XX	26-MAR-1999; 99WO-US06641.				
XX	27-MAR-1999; 98US-0079751.				
XX	(USSH) US DEPT HEALTH & HUMAN SERVICES.				
XX	Newton DL, Rybak SM;				
XX	WPI; 1999-610847/52.				
DR	N-PSDB; AA208127.				
XX	New recombinant ribonucleases, used for killing target cells, e.g. for				
PT	treating cancers, viral infections or autoimmune diseases				
XX	Claim 4; Page 59; 71pp; English.				
XX	The present sequence is a recombinant Rana pipiens ribonuclease protein				
CC	(RaPLR1) with Met at position 1 attached to (His)6 tag and Met24Leu.				
CC	Carboxy terminal end of recombinant RaPLR1 has a covalently bound ligand				
CC	binding moiety, which can be a LL2 antibody directed against CD22 on				
CC	cancerous B cells or human chorionic gonadotrophin (hCG) effective				
CC	against Kaposi's sarcoma cells. Recombinant ribonucleases can be				
CC	expressed in bacteria without an N-terminal methionine due to the				
CC	presence of a signal peptide that is cleaved by bacteria. The soluble				
CC	expression of ribonuclease allows the proteins to be fused in-frame with				
CC	ligand binding moieties to form cytotoxic fusion proteins. They can be				
CC	used for treatment of cancer and autoimmune diseases.				
XX	SQ Sequence 105 AA;				

Query Match		46.7%;	Score 283.5;	DB 20;	Length 105;
Best Local Similarity		49.1%;	Pred. No. 9.8e-25;		
Matches		55;	Conservative 16;	Mismatches 32;	Indels 9; Gaps 4;
QY	1	MONWATFOQKHINT-PIICNTIMDNNIYVGGQCKRVNTFISSATTVKAICTGVI-NM	58		
DB	1	MDMLTFQKHGVTNRDVCNNILSTNLF-...HCKDKNTFIYSRPEPVKAICKGIIASK	56		
QY	59	NVLSTTRFQNLCTRTSITPRPCPYSSRTETNYICVKCENQYVHPFAGIGRC	110		
DB	57	NVLTTSEFVSLDC---NVTSPCKYKLLKSTNKFVTCENQAPVHPFVGVRG	105		
RESULT 11					
AAV39400					
ID	AAV39400	standard; Protein; 105 AA.			
XX	AC	AAV39400;			
XX	DT	01-DEC-1999 (first entry)			
XX	DE	Recombinant frog Onconase.			
XX	KW	Ribonuclease; protein synthesis; inhibition; cancer; cytotoxic.			
XX	OS	Rana pipiens.			
XX	PN	WO9946389-A1.			
XX	PD	16-SEP-1999.			
XX	PF	11-MAR-1999; 99WO-US04252.			
XX	PR	11-MAR-1998; 98US-0077557.			
XX	PA	(IMMU-) IMMUNOMEDICS INC.			
XX	PI	Goldenberg DM, Hansen H, Leung S;			
XX	DR	WPI; 1999-551416/46.			
XX	DR	N-PSDB; AA219767.			
XX	PT	A new recombinant Onconase used to treat, e.g. colon cancer			
XX	PS	Example 1; Fig 1; 42pp; English.			
XX	CC	This sequence represents recombinant frog Onconase. Onconase has			
CC	ribonuclease and anti-tumour activity. The cDNA was produced via PCR				
CC	(using primers AA219768-219769) of two synthetic DNAs whose sequences				
CC	encoded most of the N-terminal or the C-terminal amino acids of mature				
CC	Onconase. The two PCR products generated encoded either the N-terminal				
CC	54 amino acids (minus the initial methionine) or the C-terminal 51 amino				
CC	acids, and were ligated in frame at an NruI site. The cDNA was then				
CC	subcloned into a vector e.g., pBluescript, where the ATG initiation				
CC	codon was ligated to the cDNA. After expression in E. coli, the				
CC	recombinant protein was purified. The initial N-formyl methionine was				
CC	cleaved off and the now N-terminal glutamate residue cyclised to form an				
CC	N-terminal pyroglutamate. The pyroglutamate residue forms part of the				
CC	phosphate binding pocket of Onconase and is essential for both				
CC	ribonuclease and anti-tumour activity. Onconase is a 12 kD ribonuclease				
CC	which causes cell death as a result of potent inhibition of protein				
CC	synthesis by a mechanism involving inactivation of cellular RNA. It is				
CC	not inhibited by mammalian placental ribonuclease inhibitor, which may				
CC	explain its enhanced cytotoxicity relative to mammalian enzymes. It has				
CC	anti-tumour activity against a variety of solid tumours e.g. colon or				
CC	pancreatic cancers, and can be used alone or in combination with other				
CC	anti-cancer agents such as tamoxifen. When used as an anti-tumour agent,				
CC	Onconase can be conjugated to a marker which targets it to a specific				
CC	cell type.				
XX	SQ Sequence 105 AA;				

Db 57 NVLTSEFYLSDC---NVTSPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 105

RESULT 14
AAV28879
ID AAV28879 standard; Protein; 127 AA.
XX
AC AAY28879;
XX
DT 25-JAN-2000 (first entry)
XX
DE Rana pipiens Clone 5a1b ribonuclease.
XX
KW Rana pipiens ribonuclease Clone 5a1b; RnPLR1; covalently bound; RNase;
LL2 antibody; ligand binding moiety; CD22; cancerous B cell; onconase;
KW Kaposi's Sarcoma; human chorionic gonadotropin; HCG; cancer;
KW recombinant ribonuclease; frog; signal peptide; cytotoxic fusion protein;
autoimmune disease.
XX
OS Rana pipiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..23
FT /label= Signal peptide
FT /note= "Putative"
FT Protein 24..127
FT /label= Rana_pipiens_Clone_5a1b_ribonuclease
XX
PN WO9950398-A2.
XX
PD 07-OCT-1999.
XX
PF 26-MAR-1999; 99WO-US06641.
XX
PR 27-MAR-1998; 98US-0079751.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Newton DL, Rybak SM;
XX
DR WPI; 1999-610847/52.
DR N-PSDB; AAZ08136.
XX
PT New recombinant ribonucleases, used for killing target cells, e.g. for
treating cancers, viral infections or autoimmune diseases -
XX
PS Disclosure; Page 69; 71pp; English.
XX
CC The present sequence is a Rana pipiens Clone 5a1b ribonuclease (RnPLR1).
It is encoded by Clone 5a1b cDNA obtained from Rana pipiens liver mRNA
library. It exhibits differences with Onconase (RTM) at amino acid
residues 11, 20, 85 and 103. Carboxy terminal end of RnPLR1 has a
covalently bound ligand binding moiety, which can be a L12 antibody
directed against CD22 on cancerous B cells or human chorionic
gonadotropin (hCG) effective against Kaposi's Sarcoma cells. Recombinant
ribonucleases can be expressed in bacteria without an N-terminal
methionine due to the presence of a signal peptide that is cleaved by
bacteria. The soluble expression of ribonuclease allows the proteins to
be fused in-frame with ligand binding moieties to form cytotoxic fusion
proteins. They can be used for treatment of cancer and autoimmune
diseases.
XX
SQ Sequence 127 AA;
Query Match 46.4%; Score 281.5; DB 20; Length 127;
Best Local Similarity 49.5%; Pred. No. 2.1e-24;
Matches 55; Conservative 15; Mismatches 32; Indels 9; Gaps 4;
QY 2 QNWATFOQKHINT-PIICNTIMDNNIYVGGQCKRVNTFTFISSATTVKAICTGVI-NMN 59
Db 24 QDWLTFQKKHLTNTRDVCNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIASKN 79
QY 60 VLSTTRFQNLCTRTSITPRPCYSRSTETNYICVKCENQYPVHFAGIGRC 110

Db 80 VLITSEFYLSDC---NVTSPCKYKLLKSTNTFCVTCENQAPVHFVGVGHC 127

RESULT 15
AAW35123
ID AAW35123 standard; Protein; 105 AA.
XX
AC AAW35123;
XX
DT 20-APR-1998 (first entry)
XX
DE R. pipiens recombinant RNase protein [Met-(-1)]rOnc.
XX
KW RNase A; ribonuclease; cytotoxic; onconase; nOnc; immunofusion;
tumour cell growth; frog.
XX
OS Rana pipiens.
XX
PN WO9731116-A2.
XX
PD 28-AUG-1997.
XX
PF 19-FEB-1997; 97WO-US02588.
XX
PR 21-FEB-1996; 96US-0011800.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Boque L, Newton DL, Rybak SM, Wlodawer A;
XX
DR WPI; 1997-435168/40.
DR N-PSDB; AAT94959.
XX
PT Ribonuclease molecules based on native Onconase - used for killing
cells, particularly tumour cells
XX
PS Disclosure; Pages 65-66; 90pp; English.
XX
CC AAW35115 to AAW35123 encode recombinant proteins (rOnc) which are
modifications of the RNase Onconase (RTM) (nOnc). Such novel
ribonuclease molecules are highly cytotoxic and can be used alone or to
form chemical conjugates or to target recombinant immunofusions. They are
used particularly for decreasing tumour cell growth. They can also be
used for cell separation in vitro by selectively killing unwanted types
of cells, e.g. in bone marrow prior to transplantation into a patient
undergoing marrow ablation by radiation, or for killing leukaemia cells
or T-cells that would cause graft versus host disease. The toxins can
also be used to selectively kill unwanted cells in culture. The new
ribonucleases have increased cytotoxic activity compared to nOnc and also
lower immunogenicity in humans.
XX
SQ Sequence 105 AA;
Query Match 46.0%; Score 279.5; DB 18; Length 105;
Best Local Similarity 49.1%; Pred. No. 2.9e-24;
Matches 55; Conservative 16; Mismatches 32; Indels 9; Gaps 4;
QY 1 MQNWATFOQKHINT-PIICNTIMDNNIYVGGQCKRVNTFTFISSATTVKAICTGVI-NM 58
Db 1 MEDWLTFOKKHLTNTRDVCNIMSTNLF----HCKDKNTFIYSRPEPVKAICKGIASK 56
QY 59 NVLSTTRFQNLCTRTSITPRPCYSRSTETNYICVKCENQYPVHFAGIGRC 110
Db 57 NVLTSEFYLSDC---NVTSPCKYKLLKSTNTFCVTCENQAPVHFVGVGSC 105

Search completed: January 22, 2004, 12:06:23
Job time : 34.9213 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 22, 2004, 12:01:20 ; Search time 6.59176 Seconds
(without alignments)
784.758 Million cell updates/sec

Title: US-09-622-613C-19

Perfect score: 600

Sequence: 1 QNATPQQKHINTPIICNT.....ICVKCENQYVHFAGIGRCP 110

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	595.5	97.6	111	1	RNPO_RANCA
2	451	75.2	111	1	LECS_RANJA
3	370	61.7	111	1	RNPL_RANCA
4	273.5	45.6	104	1	RN30_RANPI
5	154.5	25.8	145	1	ANG3_MOUSE
6	149.5	24.9	145	1	ANGR_MOUSE
7	136.5	22.8	145	1	ANGI_MOUSE
8	131.5	21.9	124	1	RNP_EALAC
9	129.5	21.6	124	1	RNP_FIG
10	129.5	21.6	167	1	RNBR_BOVIN
11	127.5	21.2	119	1	RNP_IGUITG
12	124.5	20.8	151	1	RNBR_CAPCA
13	123.5	20.6	123	1	ANG2_BOVIN
14	123.5	20.6	141	1	RNBR_GIRCA
15	123.5	20.6	151	1	RNBR_AXIPR
16	123	20.5	146	1	ANGI_MIOIA
17	123	20.5	146	1	ANGI_SAISC
18	120	20.0	146	1	ANGI_CERAE
19	120	20.0	147	1	ANGI_PONPY
20	119.5	19.9	143	1	RNBR_SHEEP
21	119	19.8	122	1	RNP_MACRU
22	118.5	19.8	123	1	ANGI_PIG
23	118.5	19.8	124	1	RNP_ANTAM
24	118	19.7	146	1	ANGI_AOTTR
25	117	19.5	146	1	ANGI_SAGOE
26	116.5	19.4	128	1	RNP_MYOCC
27	116.5	19.4	149	1	RNP_MOUSE
28	115	19.2	146	1	ANGI_MACHU
29	114.5	19.1	128	1	RNP_CAVPO
30	114	19.0	148	1	ANGI_BOVIN
31	113.5	18.9	124	1	RNP_CAMDR
32	113.5	18.9	128	1	RNP_HORSE
33	113	18.8	147	1	ANGI_HUMAN
					P11916 rana catesb
					P18839 rana japoni
					P14626 rana catesb
					P22069 rana pipien
					P97802 mus musculu
					O64438 mus musculu
					P21570 mus musculu
					P00673 balaenopter
					P00671 sus scrofa
					P39873 bos taurus
					P80287 iguana igua
					P79351 capreolus c
					P80929 bos taurus
					Q29542 giraffa cam
					P87350 axis porcin
					Q8wn65 miopithecus
					Q8wn60 saimiri sci
					Q8wn66 cercopithec
					Q8wn67 pongo pygma
					Q29543 ovis aries
					P00686 macropus ru
					P13466 sus scrofa
					P00668 antilocapra
					Q8wn61 aotus trivi
					Q8wn62 saquinus oe
					P00676 myocastor c
					P00683 mus musculu
					Q8wn63 macaca mula
					P00679 cavia porce
					P10152 bos taurus
					P00670 camelus dro
					P00674 equus cabal
					P03950 homo sapien

ALIGNMENTS

RESULT 1

ID	RNPO_RANCA	STANDARD;	PRT;	111 AA.
AC	P11916;			
DT	01-OCT-1989 (Rel. 12, Created)			
DT	01-FEB-1994 (Rel. 28, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	Ribonuclease, oocytes (BC 3.1.27.-) (RC-RNase) (Sialic acid-binding lectin) (SBL-C).			
OS	Rana catesbeiana (Bull frog).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.			
OX	NCBI_TaxID=8400;			
RN	[1]			
RP	SEQUENCE.			
RC	TISSUE=Egg;			
RX	MEDLINE=87299649; PubMed=3304421;			
RA	Titani K., Takio K., Kuwada M., Nitta K., Sakakibara F., Kawauchi H.,			
RA	Takayanagi G., Hakomori S.;			
RT	"Amino acid sequence of sialic acid binding lectin from frog (Rana catesbeiana) eggs."			
RL	Biochemistry 26:2189-2194(1987).			
RN	[2]			
RP	CHARACTERIZATION, AND SEQUENCE OF 59-79.			
RX	MEDLINE=92220613; PubMed=1373237;			
RA	Liao Y.-D.;			
RT	"A pyrimidine-guanine sequence-specific ribonuclease from Rana catesbeiana (bullfrog) oocytes."			
RL	Nucleic Acids Res. 20:1371-1377(1992).			
RN	[3]			
RP	CHARACTERIZATION.			
RC	TISSUE=Egg;			
RX	MEDLINE=93192604; PubMed=8448385;			
RA	Nitta K., Oyama F., Oyama R., Sekiguchi K., Kawauchi H.,			
RA	Takayanagi Y., Hakomori S., Titani K.;			
RT	"Ribonuclease activity of sialic acid-binding lectin from Rana catesbeiana eggs."			
RL	Glycobiology 3:37-45(1993).			
RN	[4]			
RP	STRUCTURE BY NMR.			
RX	MEDLINE=98437383; PubMed=9761686;			
RA	Chang C.-F., Chen C., Chen Y.-C., Hom K., Huang R.-F., Huang T.H.;			
RT	"The solution structure of a cytotoxic ribonuclease from the oocytes of Rana catesbeiana (bullfrog)."			
RL	J. Mol. Biol. 283:231-244(1998).			
CC	-I- FUNCTION: Preferentially cleaves single-stranded RNA at pyrimidine residues with a 3'flanking guanine. Hydrolyzes poly(U) and poly(C) as substrates, and prefers the former. The S-lectins in frog eggs may be involved in the fertilization and development of the frog embryo. This lectin agglutinates various animal cells, including normal lymphocytes, erythrocytes, and fibroblasts of animal and human origin.			
CC	-I- SUBUNIT: Monomer.			
CC	-I- SUBCELLULAR LOCATION: Secreted.			
CC	-I- SIMILARITY: Belongs to the pancreatic ribonuclease family.			
DR	PIR; A27121; A27121.			

Q8wme8 pan troglod
P04059 proechimys
P00566 rangifer ta
Q8wn64 papio hamad
Q9jjh1 mus musculu
P31347 oryctolagus c
P00662 capreolus c
P00662 giraffa cam
P24717 cricetus
P00657 bubalus bub
Q9wuv5 peromyscus
Q9wtt5 acomys cahi

34 113 18.8 147 1 ANGI_PANTR
35 112.5 18.8 128 1 RNP_PROGU
36 109.5 18.2 124 1 RNP_RANTA
37 109.5 18.2 146 1 ANGI_PAPHA
38 109.5 18.2 148 1 RNS4_MOUSE
39 109 18.2 125 1 ANGI_RABIT
40 108.5 18.1 124 1 RNP_CAPCA
41 108.5 18.1 124 1 RNP_GIRCA
42 108.5 18.1 130 1 RNP_CRILO
43 107.5 17.9 124 1 RNP_BUBBU
44 107.5 17.9 148 1 RNP_PERLE
45 107.5 17.9 149 1 RNP_ACOCA

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DR PDB; 1BC4; 28-OCT-98.
DR InterPro; IP0001427; RNaseA.
DR Pfam; PF00074; RNaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNaseA; 1.
DR PROSITE; PS00127; RNaseA_PANCREATIC; 1.
KW Hydrolase; Nuclease; Endonuclease; Sialic acid; Lectin; 3D-structure;
KW Pyrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT ACT_SITE 10 10
FT ACT_SITE 35 35
FT ACT_SITE 103 103
FT DISULFID 19 71
FT DISULFID 34 81
FT DISULFID 52 96
FT DISULFID 93 110
FT HELIX 3 10
FT HELIX 19 23
FT TURN 26 27
FT STRAND 37 41
FT STRAND 45 51
FT TURN 52 52
FT STRAND 57 62
FT STRAND 68 73
FT STRAND 83 88
FT STRAND 92 97
FT TURN 98 99
FT STRAND 100 107
FT SEQUENCE 111 AA; 12464 MW; 0BC9E5F5729ECF4 CRC64;

Query Match 97.6%; Score 585.5; DB 1; Length 111;
Best Local Similarity 97.3%; Pred. No. 9.3e-57; Indels 1; Gaps 1;
Matches 108; Conservative 2; Mismatches 0;

QY 1 QNWATFOQKHIIPTII-CNTILDNNIYVGGQCKRVNTFIISATTVKAICTGVINLVN 59
DB 1 QNWATFOQKHIIPTIINCNTIMDNNIYVGGQCKRVNTFIISATTVKAICTGVINLVN 60

QY 60 LSTTRFQNLCTRTSITPRPCYSSTRTETNYICVKENQYVHFAGIGRCP 110
DB 61 LSTTRFQNLCTRTSITPRPCYSSTRTETNYICVKENQYVHFAGIGRCP 111

RESULT 2
LECS_RANJA STANDARD; PRT; 111 AA.
AC P18639;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Sialic acid-binding lectin (EC 3.1.27.-).
OS Rana japonica (Japanese reddish frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8402;
RN [1]_SEQUENCE AND DISULFIDE BONDS.
RP TISSUE=Egg;
RC MEDLINE=91035319; PubMed=2229005;
RA Kamiya Y., Oyama F., Oyama R., Sakakibara F., Nitta K., Kawauchi H.,
RA Takayanagi Y., Titani K.;
RT "Amino acid sequence of a lectin from Japanese frog (Rana japonica)
RT eggs.";
RL J. Biochem. 108:139-143(1990).
CC -!- FUNCTION: THE S-LECTINS IN FROG EGGS MAY BE INVOLVED IN THE
CC FERTILIZATION AND DEVELOPMENT OF THE FROG EMBRYO. THIS LECTIN
CC PREFERENTIALLY AGGLUTINATE A LARGE VARIETY OF TUMOR CELLS, BUT IT
CC DOES NOT AGGLUTINATE NON-TRANSFORMED CELLS AND ERYTHROCYTES.
CC -!- SUBUNIT: Monomer.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
DR PIR; JX0120; JX0120.

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DR HSSP; P11916; 1BC4.
DR InterPro; IP0001427; RNaseA.
DR Pfam; PF00074; RNaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNaseA; 1.
DR PROSITE; PS00127; RNaseA_PANCREATIC; 1.
KW Hydrolase; Nuclease; Endonuclease; Sialic acid; Lectin;
KW Pyrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT ACT_SITE 10 10 BY SIMILARITY.
FT ACT_SITE 35 35 BY SIMILARITY.
FT ACT_SITE 104 104 BY SIMILARITY.
FT DISULFID 19 72
FT DISULFID 34 82
FT DISULFID 52 97
FT DISULFID 94 111
FT SEQUENCE 111 AA; 12326 MW; FDEBDDF3834ED679 CRC64;

Query Match 75.2%; Score 451; DB 1; Length 111;
Best Local Similarity 77.5%; Pred. No. 3.6e-42;
Matches 86; Conservative 8; Mismatches 15; Indels 2; Gaps 2;

QY 1 QNWATFOQKHIIPTII-CNTILDNNIYVGGQCKRVNTFIISATTVKAICTGV-INLN 58
DB 1 QNWATFOQKHIIPTIINCNTIMDKSIYVGGQCKRVNTFIISATTVKAICSGASTNRN 60

QY 59 VLSTTRFQNLCTRTSITPRPCYSSTRTETNYICVKENQYVHFAGIGRCP 109
DB 61 VLSTTRFQNLCTRTSITPRPCYSSTRTETNYICVKENRLEPVPVFAGIGRCP 111

RESULT 3
RNPL_RANJA STANDARD; PRT; 111 AA.
AC P14626;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ribonuclease, liver (EC 3.1.27.5).
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]_SEQUENCE.
RP TISSUE=Liver;
RC MEDLINE=90130374; PubMed=2613682;
RA Nitta R., Katayama N., Okabe Y., Iwama M., Watanabe H., Abe Y.,
RA Okazaki T., Ohgi K., Irie M.;
RT "Primary structure of a ribonuclease from bullfrog (Rana catesbeiana)
RT liver.";
RL J. Biochem. 106:729-735(1989).
CC -!- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
CC phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
CC with 2',3'-cyclic phosphate intermediates.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
DR PIR; JX0085; JX0085.
DR HSSP; P11916; 1BC4.
DR InterPro; IP0001427; RNaseA.
DR Pfam; PF00074; RNaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNaseA; 1.
DR PROSITE; PS00127; RNaseA_PANCREATIC; 1.
KW Hydrolase; Nuclease; Endonuclease; Pyrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT ACT_SITE 10 10 BY SIMILARITY.
FT ACT_SITE 35 35 BY SIMILARITY.
FT ACT_SITE 104 104 BY SIMILARITY.
FT DISULFID 19 72
FT DISULFID 34 82
FT DISULFID 52 97
FT DISULFID 94 111
FT SEQUENCE 111 AA; 12326 MW; FDEBDDF3834ED679 CRC64;

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SQ SEQUENCE 111 AA; 12461 MW; D64BA72456C10788 CRC64;

Query Match 61.7%; Score 370; DB 1; Length 111;
Best Local Similarity 64.9%; Pred. No. 2.2e-33;
Matches 72; Conservative 10; Mismatches 27; Indels 2; Gaps 2;

Qy 1 QNWATFOOKHIIINTPII-CNTILDNNIYIVGGQCKRVNTFIISATTVKAICTGVI-NLN 58
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 QNNAKFKKHIRSTSSIDCNDTMDKAIYIVGGCKERTFIISSEDNVKAICSGVSPDK 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 59 VLSTTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 ELSTTSFKLNTCIRDSITPRPCPYHSPDNNKICVKCEKQLPVHFVGIGKC 111
|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 4
RN30_RANPI STANDARD; PRT; 104 AA.
ID RN30_RANPI STANDARD; PRT; 104 AA.
AC P22069;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE P-30 protein (EC 3.1.27.-) (Onconase).
OS Rana pipiens (Northern leopard frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Rana.
OX NCBI_TaxID=8404;
RN [1]
RP SEQUENCE.
RC TISSUE=Embryo;
RX MEDLINE=91093131; PubMed=1985896;
RA Ardelt W., Mikulski S.M., Shogen K.;
RT "Amino acid sequence of an anti-tumor protein from Rana pipiens
RT oocytes and early embryos. Homology to pancreatic ribonucleases.";
RL J. Biol. Chem. 266:245-251(1991).
RN [2]
RP 3D-STRUCTURE MODELING.
RX MEDLINE=93066156; PubMed=1438177;
RA Mosimann S.C., Johns K.L., Ardelt W., Mikulski S.M., Shogen K.,
RA James M.N.G.;
RT "Comparative molecular modeling and crystallization of P-30 protein:
RT a novel antitumor protein of Rana pipiens oocytes and early
RT embryos.";
RL Proteins 14:392-400(1992).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).
RX MEDLINE=94166079; PubMed=8120892;
RA Mosimann S.C., Ardelt W., James M.N.G.;
RT "Refined 1.7 A X-ray crystallographic structure of P-30 protein, an
RT amphibian ribonuclease with anti-tumor activity.";
RL J. Mol. Biol. 236:1141-1153(1994).
CC -1- FUNCTION: BASIC PROTEIN WITH ANTIPROLIFERATIVE/CYTOTOXIC ACTIVITY
CC AGAINST SEVERAL TUMOR CELL LINES IN VITRO, AS WELL AS ANTITUMOR
CC IN VIVO. IT EXHIBITS A RIBONUCLEASE-LIKE ACTIVITY AGAINST HIGH
CC MOLECULAR WEIGHT RIBOSOMAL RNA.
CC -1- DEVELOPMENTAL STAGE: EARLY EMBRYOS (UP TO FOUR BLASTOMERE STAGE).
CC -1- SIMILARITY: Belongs to the pancreatic ribonuclease family.
PDB; IONC; 31-JAN-94.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; RNaseA.1.
DR ProDom; PD000535; RNaseA.1.
DR SMART; SM00092; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Hydrolase; Nuclease; Endonuclease; 3D-structure;
KW Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT ACT_SITE 10 10
FT ACT_SITE 31 31
FT ACT_SITE 97 97
FT DISULFID 19 68
FT DISULFID 30 75
FT DISULFID 48 90
FT DISULFID 87 104
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FT HELIX 3 10
FT STRAND 11 12
FT HELIX 19 22
FT TURN 23 24
FT TURN 26 30
FT STRAND 33 38
FT HELIX 41 45
FT HELIX 46 48
FT TURN 49 50
FT STRAND 55 58
FT STRAND 63 70
FT TURN 74 75
FT STRAND 77 84
FT STRAND 86 91
FT TURN 92 93
FT STRAND 94 101
SQ SEQUENCE 104 AA; 11845 MW; 22A753C2F9E566B4 CRC64;

Query Match 45.6%; Score 273.5; DB 1; Length 104;
Best Local Similarity 48.6%; Pred. No. 6.1e-23;
Matches 54; Conservative 16; Mismatches 32; Indels 9; Gaps 4;

Qy 1 QNWATFOOKHIIINT-PIICNTILDNNIYIVGGQCKRVNTFIISATTVKAICTGVI-NLN 58
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 QDWLTFOKKHITNTRDVCNDINMSTNLF----HCKDKNTFIYSRPEPVKAICKGIASKN 56
|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 59 VLSTTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 57 VLTITSEFYLSDC---NVTSPCKYKLGKSTNKKFCVTCENQAPVHFVGVGSC 104
|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 5
ANG3_MOUSE STANDARD; PRT; 145 AA.
ID ANG3_MOUSE STANDARD; PRT; 145 AA.
AC P97802;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Angiogenin-3 precursor (EC 3.1.27.-) (Angiogenin-related protein 2)
DE (EP-5)
GN ANG3 OR ANGL.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX MEDLINE=97184476; PubMed=9032278;
RA Fu X., Kamps M.P.;
RT "E2a-Pbx1 induces aberrant expression of tissue-specific and
RT developmentally regulated genes when expressed in NIH 3T3
RT fibroblasts.";
RL Mol. Cell. Biol. 17:1503-1512(1997).
CC -1- FUNCTION: ANGIOGENIN INDUCES VASCULARIZATION OF NORMAL AND
CC MALIGNANT TISSUES. ABOLISHES PROTEIN SYNTHESIS BY SPECIFICALLY
CC HYDROLYZING CELLULAR TRNAs (BY SIMILARITY).
CC -1- SIMILARITY: Belongs to the pancreatic ribonuclease family.
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CC -----
CC EMBL; U72672; AAC05794.1; -.
CC HSSP; P10152; IAGI.
CC MGD; MGI:1201793; Angl.
CC InterPro; IPR001427; RNaseA.
CC Pfam; PF00074; RNaseA; 1.
CC PRINTS; PR00794; RIBONUCLEASE.
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DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNaseA; PC; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Hydrolase; Nuclease; Endonuclease; Angiogenesis;
KW Protein synthesis inhibitor; Signal; Pyrrolidone carboxylic acid.
FT SIGNAL 1 24
FT CHAIN 25 145
FT MOD_RES 25 25
FT ACT_SITE 37 37
FT ACT_SITE 64 64
FT ACT_SITE 137 137
FT DISULFID 50 104
FT DISULFID 63 115
FT DISULFID 81 130
FT DISULFID 81 130
SQ SEQUENCE 145 AA; 16696 MW; DE9D3BC92F1D682C CRC64;
Query Match 25.8%; Score 154.5; DB 1; Length 145;
Best Local Similarity 43.6%; Pred. No. 7e-10; 23; Indels 9; Gaps 4;
Matches 34; Conservative 12; Mismatches 23; Indels 9; Gaps 4;
Oy 33 CKRVNTFIISATTVKAIC-----TGVINLVLTTRFQNLNCTRTSITPR-PCPYSSR 85
Db 63 CKEVNTFHDTKNNIKALCGNGRPGV-NFRI-SNSRFQVTTCTHKGSRPPCQYNAP 120
Oy 86 TETNYICVKCENQYVPHF 103
Db 121 KDFRYIVIAECGWPVHF 138
RESULT 6
ANGR_MOUSE
ID ANGR_MOUSE STANDARD; PRT; 145 AA.
AC Q64438;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Angiogenin-related protein precursor.
GN ANGRP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129; TISSUE=liver;
RX MEDLINE=96079109; PubMed=8530072;
RA Brown W.E., Noble V., Subramanian V., Shapiro R.;
RT "The mouse angiogenin gene family: structures of an angiogenin-related
RL protein gene and two pseudogenes.";
RL Genomics 29:200-206(1995).
CC -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
DR EMBL; U22519; AAA91367.1; -.
DR HSP; P03950; 1A4Y.
DR MGD; MGI:104984; Angrp.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaseA; 1.
DR PRINTS; PR00794; RIBONUCLEASE.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNaseA; PC; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Signal; Hydrolase; Nuclease; Endonuclease;
KW Pyrrolidone carboxylic acid.
FT SIGNAL 1 24
FT POTENTIAL.
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FT CHAIN 25 145
FT MOD_RES 25 25
FT ACT_SITE 37 37
FT ACT_SITE 64 64
FT ACT_SITE 137 137
FT DISULFID 50 104
FT DISULFID 63 115
FT DISULFID 81 130
SQ SEQUENCE 145 AA; 16612 MW; 29A6EB814429C4AD CRC64;
Query Match 24.9%; Score 149.5; DB 1; Length 145;
Best Local Similarity 44.2%; Pred. No. 2.5e-09;
Matches 34; Conservative 9; Mismatches 27; Indels 7; Gaps 3;
Oy 33 CKRVNTFIISATTVKAICGV-----INLVLTTRFQNLNCTRTSITPR-PCPYSSRT 86
Db 63 CKDVNTFHDTKNNIKALCGKSGPYGNLRI-SKSRFQVTTCTHKGSRPPRCYRASK 121
Oy 87 ETNYICVKCENQYVPHF 103
Db 122 GFRYIIIGCENGWPVHF 138
RESULT 7
ANGI_MOUSE
ID ANGI_MOUSE STANDARD; PRT; 145 AA.
AC P21570;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Angiogenin precursor (EC 3.1.27.-) (Ribonuclease 5) (RNase 5).
GN ANG.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91025023; PubMed=2222458;
RA Bond M.D., Vallee B.L.;
RT "Isolation and sequencing of mouse angiogenin DNA.";
RL Biochem. Biophys. Res. Commun. 171:988-995(1990).
RN [2]
RP PARTIAL SEQUENCE.
RC TISSUE=Serum;
RX MEDLINE=93192291; PubMed=8448182;
RA Bond M.D., Strydom D.J., Vallee B.L.;
RT "Characterization and sequencing of rabbit, pig and mouse
RL angiogenins: discernment of functionally important residues and
RN regions.";
RL Biochim. Biophys. Acta 1162:177-186(1993).
CC -!- FUNCTION: MAY FUNCTION AS A TRNA-SPECIFIC RIBONUCLEASE THAT BINDS
CC TO ACTIN ON THE SURFACE OF ENDOTHELIAL CELLS; ONCE BOUND,
CC ANGIOGENIN IS ENDOCYTOSED AND TRANSLOCATED TO THE NUCLEUS, THEREBY
CC PROMOTING THE ENDOTHELIAL INVASIVENESS NECESSARY FOR BLOOD VESSEL
CC FORMATION. ANGIOGENIN INDUCES VASCULARIZATION OF NORMAL AND
CC MALIGNANT TISSUES. ABOLISHES PROTEIN SYNTHESIS BY SPECIFICALLY
CC HYDROLYZING CELLULAR TRNAs.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
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CC or send an email to license@isb-sib.ch).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the pancreatic ribonuclease family.
DR EMBL; U22516; AAA91366.1; -.
DR PIR; A35932; A35932.
DR HSP; P03950; 1A4Y.
```

MGD; MGI:88022; Ang.
 DR InterPro: IPR001427; RNaseA.
 DR Pfam: PF00074; RNaseA; 1.
 DR PRINTS: PR00794; RIBONUCLEASE.
 DR ProDom: PD000535; RNaseA; 1.
 DR SMART: SM00092; RNaseA; 1.
 DR PROSITE: PS00127; RNASE PANCREATIC; 1.
 KW Hydrolyase; Nuclease; Endonuclease; Angiogenesis;
 KW protein synthesis inhibitor; Signal; Pyrrolidone carboxylic acid.
 FT SIGNAL 1 24
 FT CHAIN 25 145
 FT MOD_RES 25 25
 FT ANGIOGENIN.
 FT PYRROLIDONE CARBOXYLIC ACID (BY
 FT SIMILARITY).
 FT ACT_SITE 37 37
 FT ACT_SITE 64 64
 FT ACT_SITE 137 137
 FT BY SIMILARITY.
 FT DISULFID 50 104
 FT BY SIMILARITY.
 FT DISULFID 63 115
 FT BY SIMILARITY.
 FT DISULFID 81 130
 FT BY SIMILARITY.
 SQ SEQUENCE 145 AA; 16228 MW; 06944260BB764938 CRC64;

Query Match 22.8%; Score 136.5; DB 1; Length 145;
 Best Local Similarity 40.3%; Pred. No. 6.3e-08;
 Matches 31; Conservative 11; Mismatches 28; Indels 7; Gaps 3;

OY 33 CKRVNTFTIISATTVAICTG-----VINLVNLTTRFQNTCTRTSITPR-PCPYSSRT 86
 DB 63 CKDVTFTIHNKSNKALCANGSPYRENLR-MSKSPQVTTCKTGSPRPPCOYRASA 121
 OY 87 ETNYICVKCENQYPVHF 103
 DB 122 GFRHVVIACENGLPVHF 138

RESULT 8
 RNP_BALAC
 ID RNP_BALAC STANDARD; PRT; 124 AA.
 AC P00673;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Ribonuclease pancreatic (EC 3.1.27.5) (Rnase 1) (Rnase A).
 GN RNASEL OR RNSL.
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Mysticeti;
 OC Balaeopteridae; Balaeoptera.
 OX NCBI_TaxID=9767;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=76277855; PubMed=962870;
 RA Emmens M., Welling G.W., Beintema J.J.;
 RT "The amino acid sequence of pike-whale (lesser-rorqual) pancreatic
 RT ribonuclease.";
 RL Biochem. J. 157:317-323(1976).
 CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
 CC phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
 CC with 2',3'-cyclic phosphate intermediates.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Pancreas
 CC -1- SIMILARITY: Belongs to the pancreatic ribonuclease family.
 DR PIR; A00818; NRWHK.
 DR HSP; P00656; 1SRN.
 DR InterPro: IPR001427; RNaseA.
 DR Pfam: PF00074; RNaseA; 1.
 DR PRINTS: PR00794; RIBONUCLEASE.
 DR ProDom: PD000535; RNaseA; 1.
 DR SMART: SM00092; RNaseA; 1.
 DR PROSITE: PS00127; RNASE PANCREATIC; 1.
 KW Hydrolyase; Nuclease; Endonuclease; Glycoprotein.
 FT DISULFID 26 84
 FT BY SIMILARITY.
 FT DISULFID 40 95
 FT BY SIMILARITY.
 FT DISULFID 58 110
 FT BY SIMILARITY.

FT DISULFID 65 72
 FT ACT_SITE 12 12
 FT BY SIMILARITY.
 FT ACT_SITE 41 41
 FT BY SIMILARITY.
 FT ACT_SITE 119 119
 FT BY SIMILARITY.
 FT CARBOHYD 76 76
 FT N-LINKED (GLCNAC. .) (30%).
 SQ SEQUENCE 124 AA; 14125 MW; F57475459F697E20 CRC64;

Query Match 21.9%; Score 131.5; DB 1; Length 124;
 Best Local Similarity 32.5%; Pred. No. 1.9e-07;
 Matches 38; Conservative 17; Mismatches 39; Indels 23; Gaps 7;

OY 6 FQOKHII-----NTPIIICNTILDNNIYIVGQCKRVNTFTIISATTVAICTGVINLV 59
 DB 8 FQHQHMDSGNSPGNNPNYCNQMMHR-KMTQGRCKPVNTFVHESLEDVKVCS---QKNV 63
 OY 60 L-----STTRFQNTCTRTSITPRP-CPYSSRTETNYICVKCE-NQY-PVHF 103
 DB 64 LCKNGRTNCTYESNSTMHTDCRQTGSSKYPNCAVYKTSQEKHII1VACEGNPVVPHF 120

RESULT 9
 RNP_FIG
 ID RNP_FIG STANDARD; PRT; 124 AA.
 AC P00671;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Ribonuclease pancreatic (EC 3.1.27.5) (Rnase 1) (Rnase A).
 GN RNASEL OR RNSL.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=70104197; PubMed=5460946;
 RA Jackson R.L., Hirs C.H.W.;
 RT "The primary structure of porcine pancreatic ribonuclease. II. The
 RT amino acid sequence of the reduced S-aminoethylated protein.";
 RL J. Biol. Chem. 245:637-653(1970).
 RN [2]
 RP REVISION TO 2.
 RA Wieringa R.K., Huizinga J.D., Gaastra W., Welling G.W., Beintema J.J.;
 RT "Affinity chromatography of porcine pancreatic ribonuclease and
 RT reinvestigation of the N-terminal amino acid sequence.";
 RL FEBS Lett. 31:181-185(1973).
 RN [3]
 RP DISULFIDE BONDS.
 RX MEDLINE=70104198; PubMed=4904878;
 RA Phelan J.J., Hirs C.H.W.;
 RT "The primary structure of porcine pancreatic ribonuclease. 3. The
 RT disulfide bonds.";
 RL J. Biol. Chem. 245:654-661(1970).
 CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to nucleoside 3'-
 CC phosphates and 3'-phosphooligonucleotides ending in C-P or U-P
 CC with 2',3'-cyclic phosphate intermediates.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Pancreas.
 CC -1- SIMILARITY: Belongs to the pancreatic ribonuclease family.
 DR PIR; A92071; NREG.
 DR HSP; P00656; 1SRN.
 DR InterPro: IPR001427; RNaseA.
 DR Pfam: PF00074; RNaseA; 1.
 DR PRINTS: PR00794; RIBONUCLEASE.
 DR ProDom: PD000535; RNaseA; 1.
 DR SMART: SM00092; RNaseA; 1.
 DR PROSITE: PS00127; RNASE PANCREATIC; 1.
 KW Hydrolyase; Nuclease; Endonuclease; Glycoprotein.
 FT DISULFID 26 84
 FT DISULFID 40 95
 FT DISULFID 58 110
 FT DISULFID 65 72
 FT BY SIMILARITY.
 FT ACT_SITE 12 12

Db 122 G 122

Search completed: January 22, 2004, 12:02:09
Job time : 6.59176 secs

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OM protein - protein search, using sw model

Run on: January 22, 2004, 12:01:20 ; Search time 12.3596 Seconds
(without alignments)
855.901 Million cell updates/sec

Title: US-09-622-613C-19
Perfect score: 600
Sequence: 1 QNWATFQKHINTPIICNT.....ICVKCENQYPVHFAGIGRCP 110

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_76:*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	582.5	97.1	111	2 A27121	ribonuclease-relat
2	451	75.2	111	1 JX0120	ribonuclease-relat
3	370	61.7	111	2 JX0085	pancreatic ribonuc
4	270.5	45.1	104	2 A39035	ribonuclease-relat
5	136.5	22.8	145	1 A35932	angiogenin precurs
6	131.5	21.9	124	1 NRWHK	pancreatic ribonuc
7	129.5	21.6	124	1 NRPFG	pancreatic ribonuc
8	129.5	21.6	167	2 S20066	pancreatic-type ri
9	127.5	21.2	119	2 S41111	pancreatic ribonuc
10	119	19.8	122	1 NKRGR	pancreatic ribonuc
11	118.5	19.8	123	1 A43825	angiogenin - pig
12	118.5	19.8	124	1 NRPFH	pancreatic ribonuc
13	116.5	19.4	128	1 NRCU	pancreatic ribonuc
14	116.5	19.4	149	1 NRMS	pancreatic ribonuc
15	114.5	19.1	128	1 NRGPB	pancreatic ribonuc
16	114	19.0	125	1 A32474	pancreatic (valida
17	113.5	18.9	124	1 NRCM	pancreatic ribonuc
18	113.5	18.9	124	1 NRCM	pancreatic ribonuc
19	113.5	18.9	124	1 NRCMB	pancreatic ribonuc
20	113.5	18.9	128	1 NRHO	pancreatic ribonuc
21	113	18.8	147	1 NRHUAG	angiogenin precurs
22	112.5	18.8	128	1 NRKS	pancreatic ribonuc
23	110.5	18.4	124	2 S08549	ribonuclease - dom
24	109.5	18.2	124	1 NRDEN	pancreatic ribonuc
25	109	18.2	125	1 B43825	angiogenin - rabbi
26	108.5	18.1	124	1 NRGF	pancreatic ribonuc
27	108.5	18.1	124	1 NRDEO	pancreatic ribonuc
28	108.5	18.1	130	2 S22808	pancreatic ribonuc
29	107.5	17.9	124	1 NRWB	pancreatic ribonuc

30	107.5	17.9	158	2 I61900	eosinophil-derived
31	106.5	17.8	124	1 NRBOB	pancreatic ribonuc
32	106.5	17.8	124	1 NREKN	pancreatic ribonuc
33	106.5	17.8	124	2 S07141	pancreatic ribonuc
34	106.5	17.8	150	1 NRBO	pancreatic ribonuc
35	105.5	17.6	119	2 JX0115	pancreatic ribonuc
36	105.5	17.6	124	1 NRSH	pancreatic ribonuc
37	105.5	17.6	152	1 NRRT	pancreatic ribonuc
38	104.5	17.4	124	1 NRCEB	pancreatic ribonuc
39	103.5	17.2	125	4 A47498	seminal ribonuclea
40	103.5	17.2	150	1 NRBOB	pancreatic ribonuc
41	102.5	17.1	124	1 NRHP	pancreatic ribonuc
42	101	16.8	125	2 S04503	pancreatic ribonuc
43	100.5	16.8	124	1 NRGN	pancreatic ribonuc
44	100.5	16.8	124	1 NRDEF	pancreatic ribonuc
45	100.5	16.8	124	2 S08546	pancreatic ribonuc

ALIGNMENTS

RESULT 1

A27121 ribonuclease-related sialic acid-binding lectin - bullfrog

C:Species: Rana catesbeiana (bullfrog)

C:Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 30-Jun-1993

C:Accession: A27121

R:Titani, K.; Takio, K.; Kuwada, M.; Nitta, K.; Sakakibara, F.; Kawachi, H.; Takayanagi,

Biochemistry 26, 2189-2194, 1987

A:Title: Amino acid sequence of sialic acid-binding lectin from frog (Rana catesbeiana)

A:Reference number: A27121; MUID:87299649; PMID:3304421

A:Accession: A27121

A:Molecule type: protein

A:Residues: 1-111 <TIR>

C:Superfamily: pancreatic ribonuclease

C:Keywords: lectin

Query Match 97.1%; Score 582.5; DB 2; Length 111;
Best Local Similarity 96.4%; Pred. No. 1e-50;
Matches 107; Conservative 3; Mismatches 0; Indels 1; Gaps 1;

Qy	1	QNWATFQKHINTPII-CNTILDNNIYVGGQCKRVNTFISSATTVAICTGVINLNV	59
Db	1	ENWATFQKHINTPIINCNTIMDNNIYVGGQCKRVNTFISSATTVAICTGVINNV	60
Qy	60	LSTTRFQNTCTRTSITPRCPYSSRTETNYICVKCENQYPVHFAGIGRCP	110
Db	61	LSTTRFQNTCTRTSITPRCPYSSRTETNYICVKCENQYPVHFAGIGRCP	111

RESULT 2

JX0120 ribonuclease-related sialic acid-binding lectin - Japanese frog

C:Species: Rana japonica (Japanese frog)

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C:Accession: JX0120

R:Kamiya, Y.; Oyama, F.; Oyama, R.; Sakakibara, F.; Nitta, K.; Kawachi, H.; Takayanagi,

J. Biochem. 108, 139-143, 1990

A:Title: Amino acid sequence of a lectin from Japanese frog (Rana japonica) eggs.

A:Reference number: JX0120; MUID:91035319; PMID:2229005

A:Accession: JX0120

A:Molecule type: protein

A:Residues: 1-111 <KAM>

A:Experimental source: egg

C:Superfamily: pancreatic ribonuclease

C:Keywords: lectin; pyrrolidone carboxylic acid

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F:19-72,34-82,52-97,94-111/Disulfide bonds: #status experimental

Query Match 75.2%; Score 451; DB 1; Length 111;

Best Local Similarity 77.5%; Pred. No. 1.e-37;

Matches 86; Conservative 8; Mismatches 15; Indels 2; Gaps 2;

Qy	1	QNWATFOQKHINTP-IICNTILDNNIYVGGQCKRVNTFFIISATTVAICTGV-INLN	58
Db	1	QNWAKFOEKHINTSNINCNTIMDKSIYVGGQCKERTNTFIISATTVAICSGASTNRN	60
Qy	59	VLSTTRFOLNCTRTSITRPPCPYSSRTETNYICVKENQVPHFAGIGRC	109
Db	61	VLSTTRFOLNCTRSATAPRCPYNSRTETNYICVKENRULPVHPAGIGRC	111
RESULT 3			
JX0085			
pancreatic ribonuclease (EC 3.1.27.5) - bullfrog			
C:Species: Rana catesbeiana (bullfrog)			
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 05-Aug-1994			
C:Accession: JX0085			
J:Biochem. 106, 729-735, 1989			
R:Nitta, R.; Katayama, N.; Okabe, Y.; Iwama, M.; Watanabe, H.; Abe, Y.; Okazaki, T.; Ohg			
A:Title: Primary structure of a ribonuclease from bullfrog (Rana catesbeiana) liver.			
A:Reference number: JX0085; MUID:90130374; PMID:2613682			
A:Accession: JX0085			
A:Molecule type: protein			
A:Residues: 1-111 <NIT>			
C:Superfamily: pancreatic ribonuclease			
C:Keywords: hydrolase; pyroglutamic acid			
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental			
F:10.35.104/Active site: His, Lys, His #status predicted			
F:19.72.34-82,52-97,94-111/Disulfide bonds: #status predicted			
Query Match 61.7%; Score 370; DB 2; Length 111;			
Best Local Similarity 64.9%; Pred. No. 1.1e-29;			
Matches 72; Conservative 10; Mismatches 27; Indels 2; Gaps 2;			
Qy	1	QNWATFOQKHINTPIL-CNTILDNNIYVGGQCKRVNTFFIISATTVAICTGVI-NLN	58
Db	1	QNWAKFOEKHIRSTSSICNTIMDKAIYVGGQCKERTNTFIISDNDVKAICSGVSPDRK	60
Qy	59	VLSTTRFOLNCTRTSITRPPCPYSSRTETNYICVKENQVPHFAGIGRC	109
Db	61	ELSTTSFKLNTCIRDSITRPPCPYHSPDNNKICVKCEKQLPVHPVGIGKC	111
RESULT 4			
A39035			
ribonuclease-related anti-tumor protein - northern leopard frog (fragment)			
C:Species: Rana pipiens (northern leopard frog)			
C:Date: 31-Jul-1991 #sequence_revision 31-Jul-1991 #text_change 30-Jun-1993			
C:Accession: A39035			
R:Ardelet, W.; Mikulski, S.M.; Shogen, K.			
J: Biol. Chem. 266, 245-251, 1991			
A:Title: Amino acid sequence of an anti-tumor protein from Rana pipiens oocytes and earl			
A:Reference number: A39035; MUID:91093131; PMID:1985896			
A:Accession: A39035			
A:Status: preliminary			
A:Molecule type: protein			
A:Residues: 1-104 <ARD>			
C:Superfamily: pancreatic ribonuclease			
Query Match 45.1%; Score 270.5; DB 2; Length 104;			
Best Local Similarity 47.7%; Pred. No. 7.2e-20;			
Matches 53; Conservative 17; Mismatches 32; Indels 9; Gaps 4;			
Qy	1	QNWATFOQKHINT-PIICNTILDNNIYVGGQCKRVNTFFIISATTVAICTGVI-NLN	58
Db	1	EDWLTFQKHINTRDVDCDNI MSTNLF----HCKDKNTFIYSRPEPVKAICKGLIASKN	56
Qy	59	VLSTTRFOLNCTRTSITRPPCPYSSRTETNYICVKENQVPHFAGIGRC	109
Db	57	VLTTSEFVLSDC---NVTSRPKYKGLKSTNKCFCVTCENQAPVHPVGVC	104
RESULT 5			
A35932			
angiogenin precursor - mouse			

N:Alternate names: angiogenesis factor			
N:Contains: ribonuclease (EC 3.1.27.-)			
C:Species: Mus musculus (house mouse)			
C:Date: 09-Nov-1990 #sequence_revision 09-Nov-1990 #text_change 18-Jun-1999			
C:Accession: A35932			
R:Bond, M.D.; Vallee, B.L.			
Biochem. Biophys. Res. Commun. 171, 988-995, 1990			
A:Title: Isolation and sequencing of mouse angiogenin DNA.			
A:Reference number: A35932; MUID:91025023; PMID:2222458			
A:Accession: A35932			
A:Status: not compared with conceptual translation			
A:Molecule type: DNA			
A:Residues: 1-145 <BON>			
A:Cross-references: GB:U22516; NID:9726325; PIDN:AAA91366.1; PID:9726326			
C:Genetics:			
A:Introns: #status absent			
C:Function:			
A:Description: hydrolyzes tRNA; induces vascularization of normal and malignant tissues			
C:Superfamily: pancreatic ribonuclease			
C:Keywords: angiogenesis; hydrolase; nucleic acid degradation; pyroglutamic acid			
F:1-24/Domain: signal sequence #status predicted <SIG>			
F:25-145/Product: angiogenin #status predicted <MAT>			
F:25/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted			
F:37.64.137/Active site: His, Lys, His #status predicted			
F:50-104,63-115,81-130/Disulfide bonds: #status predicted			
Query Match 22.8%; Score 136.5; DB 1; Length 145;			
Best Local Similarity 40.3%; Pred. No. 1.8e-06;			
Matches 31; Conservative 11; Mismatches 28; Indels 7; Gaps 3;			
Qy	33	CKRVNTFIISATTVAICTG-----VINLNVLTTRFOLNCTRTSITPR-PCPYSSRT	86
Db	63	CKDVTTFIHGNSKNIKKAICGANGSPYRENLR-MSKSPFQVTTCKTGTSRPPCQYRASA	121
Qy	87	ETNYICVKENQYVPVFH	103
Db	122	GFRHWIACENGLPVHF	138
RESULT 6			
NRWHK			
pancreatic ribonuclease (EC 3.1.27.5) - minke whale			
N:Alternate names: RNase 1; RNase A			
C:Species: Balaenoptera acutorostrata (minke whale, lesser rorqual)			
C:Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 03-Jun-1994			
C:Accession: A00818			
R:Emmens, M.; Welling, G.W.; Beintema, J.J.			
Biochem. J. 157, 317-323, 1976			
A:Title: The amino acid sequence of pike whale (lesser rorqual) pancreatic ribonuclease.			
A:Reference number: A00818; MUID:76277855; PMID:962870			
A:Accession: A00818			
A:Molecule type: protein			
A:Residues: 1-124 <EMM>			
C:Superfamily: pancreatic ribonuclease			
C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas			
F:12.41.119/Active site: His, Lys, His #status predicted			
F:26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted			
F:76/Binding site: carbohydrate (Aen) (covalent) (partial) #status experimental			
Query Match 21.9%; Score 131.5; DB 1; Length 124;			
Best Local Similarity 32.5%; Pred. No. 4.9e-06;			
Matches 38; Conservative 17; Mismatches 39; Indels 23; Gaps 7;			
Qy	6	FQKHII-----NTPPICNTILDNNIYVGGQCKRVNTFIISATTVAICTGVINLV	59
Db	8	FQKHII-----NTPPICNTILDNNIYVGGQCKRVNTFIISATTVAICTGVINLV	59
Qy	60	L-----STTRFOLNCTRTSITPR-CPYSSRTETNYICVKE-NQY-PVHF	103
Db	64	LCKNGRTNCTYESNTMTIDCRQTGSSKYPNCAVKTQKXHIIVACSGNPVYPVHF	120
RESULT 7			

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Query Match      21.6%; Score 129.5; DB 2; Length 167;
Best Local Similarity 30.6%; Pred. No. 1e-05;
Matches 37; Conservative 18; Mismatches 43; Indels 23; Gaps 7;

QY 4 ATFOQKH-----INTPIICNTLDNNIYIVGGCKRVNTFISSATTVKAICTGVINL 57
DB 32 AKFRROHMDGSSSSSNPNYCNOMKRR-RMTHGRCKPVNTFVHSLDDVKAVC-----QK 87
QY 58 NVL-----STTRFOLNTCTRTSITPRP-CRYSRSTETNYICVKCE-NOY-PVHFA 104
DB 88 NITCKNGHPNCYQSKSTMSITDCRETGSSKYPCAAYKTSQKQKIYTVACEGPNYPVPHD 147
QY 105 G 105
DB 148 G 148

RESULT 9
S4111
Paucratric ribonuclease - common iguana
C:Species: Iguana iguana (common iguana)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 21-Aug-1998
C:Accession: S4111
R:Zhao, W.; Beintema, J.J.; Hofsteenge, J.
Eur. J. Biochem. 219, 641-646, 1994
A:Title: The amino acid sequence of iguana (Iguana iguana) pancreatic ribonuclease.
A:Reference number: S4111; MUID:94139745; PMID:8307028
A:Accession: S4111
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-119 <ZHA>
C:Superfamily: pancreatic ribonuclease

Query Match      21.2%; Score 127.5; DB 2; Length 119;
Best Local Similarity 29.6%; Pred. No. 1.2e-05;
Matches 34; Conservative 17; Mismatches 51; Indels 13; Gaps 4;

QY 1 QNWATFOQKH-----INTPIICNTLDNNIYIVGGCKRVNTFISSATTVKAIC-- 51
DB 1 QDWSFGQKHIDYPTSASNPWAYCDLMMQRR-NUNPTKCKTRNTFVHASPSEIQOVCGS 59
QY 52 --TGVINLVLSITTRFOLNTCTRTSIT-PRCPYSRSTETNYICVKCENQYPVHF 103
DB 60 GCETHEDNLYDSNESFDLTDCKNVGGTAPSSCKYNGTPTKRIACENNPVHF 114

RESULT 10
NRKGR
pancreatic ribonuclease (EC 3.1.27.5) - red kangaroo
N:Alternate names: RNase A
C:Species: Macropus rufus, Megaleia rufa (red kangaroo)
C:Date: 30-Nov-1980 #sequence_revision 30-Nov-1980 #text_change 04-Oct-1996
C:Accession: A00833
R:Gaastra, W.; Wellington, G.W.; Beintema, J.J.
Eur. J. Biochem. 86, 209-217, 1978
A:Title: The amino-acid sequence of kangaroo pancreatic ribonuclease.
A:Reference number: A00833; MUID:78190621; PMID:658039
A:Accession: A00833
A:Molecule type: protein
A:Residues: 1-122 <GAA>
C:Superfamily: pancreatic ribonuclease
C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas
F:11,40,117/Active site: His, Lys, His #status predicted
F:25-83,39-94,57-109,64-71/Diulfide bonds: #status predicted
F:61/Binding site: carbohydrate (Asn) (covalent) #status absent

Query Match      19.8%; Score 119; DB 1; Length 122;
Best Local Similarity 29.8%; Pred. No. 8.2e-05;
Matches 34; Conservative 17; Mismatches 45; Indels 18; Gaps 6;

QY 6 FOQKH-----INTPIICNTLDNNIYIVGGCKRVNTFISSATTVKAIC----- 51
DB 32 AKFRROHMDGSSSSSNPNYCNOMKRR-RMTHGRCKPVNTFVHSLDDVKAVC-----QK 87
QY 58 NVL-----STTRFOLNTCTRTSITPRP-CRYSRSTETNYICVKCE-NOY-PVHFA 104
DB 88 NITCKNGHPNCYQSKSTMSITDCRETGSSKYPCAAYKTSQKQKIYTVACEGPNYPVPHD 147
QY 105 G 105
DB 148 G 148

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Db 7 FQRQHMDTEHSTASSSNYNLMMKAR-DWTSGRCKPLNTFTIHEPKSVVDVACHQENVTCK 65

Qy 52 TGVINLNLVSTTRFQNLCTRTSITPRP-CPYSSRTETNYICVKENQY-PVHF 103

Db 66 NGRNTNC-YKSNRSLITNCROTGASKYPNCQVETSNLKNKIIVACEGQYVPVHF 118

RESULT 11

A43825

C:Species: Sus scrofa domestica (domestic pig)

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999

C:Accession: S29834; A43825

R:Bond, M.D.; Strydom, D.J.; Vallee, B.L.

Biochim. Biophys. Acta 1162, 177-186, 1993

A:Title: Characterization and sequencing of rabbit, pig and mouse angiogenins: discernme

A:Reference number: S29833; MUID:93192291; PMID:8446182

A:Accession: S29834

A:Status: Preliminary

A:Molecule type: protein

A:Residues: 1-123 <BON>

A:Note: this sequence was submitted to the Protein Sequence Database, December 1992

C:Superfamily: pancreatic ribonuclease

Query Match 19.8%; Score 118.5; DB 1; Length 123;

Best Local Similarity 39.5%; Pred. No. 9.3e-05;

Matches 30; Conservative 6; Mismatches 35; Indels 5; Gaps 2;

Qy 33 CKRVNTFTFISSATTVKAICTG----VINLNLVSTTRFQNLCTRTSITPR-PCPYSSRTE 87

Db 39 CKEVNTFTGTRNDIKAIKCNKNGEPYNNFRSRKSPFQITTCCKHKGGSNRPPCGVRATAG 98

Qy 88 TNYICVKENQYVPVHF 103

Db 99 FRTIIVACENGLPVHF 114

RESULT 12

NRPBH

pancreatic ribonuclease (EC 3.1.27.5) - pronghorn (tentative sequence)

N:Alternate names: RNase 1; RNase A

C:Species: Antilocapra americana (pronghorn)

C:Date: 28-Feb-1981 #sequence_revision 28-Feb-1981 #text_change 31-Mar-2000

C:Accession: A00813

R:Beintema, J.J.; Gaastera, W.; Munniksma, J.

J. Mol. Evol. 13, 305-316, 1979

A:Title: Primary structure of pronghorn pancreatic ribonuclease: close relationship betw

A:Reference number: A00813; MUID:80075014; PMID:513141

A:Accession: A00813

A:Molecule type: protein

A:Residues: 1-124 <BEI>

C:Superfamily: pancreatic ribonuclease

C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas

F:12.41.119/Active site: His, Lys, His #status predicted

F:26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted

F:34/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental

Query Match 19.8%; Score 118.5; DB 1; Length 124;

Best Local Similarity 29.9%; Pred. No. 9.4e-05;

Matches 35; Conservative 19; Mismatches 44; Indels 19; Gaps 7;

Qy 4 ATFFQKHINTPI-----ICNTILDNNIYVGGCKRVNTFTFISSATTVKAICT----- 52

Db 6 AKFERQHIDSNFSSVSSSNYNQNMKSR-NLTQGRCKPVNTFVHESLADVQAVCSQKNVA 64

Qy 53 ---GVINLNLVSTTRFQNLCTRTSITPRP-CPYSSRTETNYICVKCE-NQY-PVHF 103

Db 65 CKNGQTC-NQYSYMTSITDCRETGSSKYPNCAYKTQAKHIIIVACEGNPVPVHY 120

RESULT 13

NRCU

pancreatic ribonuclease (EC 3.1.27.5) - nutria (tentative sequence)

N:Alternate names: RNase 1; RNase A

C:Species: Myocastor coypus (nutria, coypu)

C:Date: 24-Apr-1984 #sequence_revision 30-Sep-1988 #text_change 31-Mar-2000

C:Accession: A00822

R:van den Berg, A.; van den Hende-Timmer, L.; Beintema, J.J.

Biochim. Biophys. Acta 453, 400-409, 1976

A:Title: Isolation, properties and primary structure of coypu and chinchilla pancreatic ;

A:Reference number: A0612; MUID:77065676; PMID:999896

A:Accession: A00822

A:Molecule type: protein

A:Residues: 1-128 <VAN>

C:Superfamily: pancreatic ribonuclease

C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas

F:12.41.119/Active site: His, Lys, His #status predicted

F:26-84,40-95,58-110,65-72/Disulfide bonds: #status predicted

F:34/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 19.4%; Score 116.5; DB 1; Length 128;

Best Local Similarity 30.8%; Pred. No. 0.00015;

Matches 36; Conservative 16; Mismatches 42; Indels 23; Gaps 7;

Qy 6 FQQRKH-----INTPICNTILDNNIYVGGCKRVNTFTFISSATTVKAICTGVINLNV 59

Db 8 FERQHMDSRGSPSTNPNYCNEMKSR-NMTQGRCKPVNTFVHEPLADVQAVC---FQKNV 63

Qy 60 L-----STTRFQNLCTRTSITPRP-CPYSSRTETNYICVKCE-NQY-PVHF 103

Db 64 LCKNGQTCYOSNSNMHITDCRVTSNDYPNCSYRSTOEEKSIIVACEGNPVPVHF 120

RESULT 14

NRMS

pancreatic ribonuclease (EC 3.1.27.5) precursor - mouse

N:Alternate names: RNase 1; RNase A

C:Species: Mus musculus (house mouse)

C:Date: 30-Nov-1980 #sequence_revision 13-Mar-1997 #text_change 18-Jun-1999

C:Accession: A34090; S22598; A00830

R:Schueller, C.; Nijssen, H.M.J.; Kok, R.; Beintema, J.J.

Mol. Biol. Evol. 7, 29-44, 1990

A:Title: Evolution of nucleic acids coding for ribonucleases: the mRNA sequence of mouse

A:Reference number: A34090; MUID:90136034; PMID:2299980

A:Accession: A34090

A:Status: Preliminary

A:Molecule type: mRNA

A:Residues: 1-149 <SCH>

A:Cross-references: GB:M27814; MID:g200762; PIDN:AAA40060.1; PID:g200763

R:Samuelson, L.C.; Wiebauer, K.; Howard, G.; Schmid, R.M.; Koeplin, D.; Meisler, M.H.

Nucleic Acids Res. 19, 6935-6941, 1991

A:Title: Isolation of the murine ribonuclease gene Rib-1: structure and tissue specific

A:Reference number: S22598; MUID:92107684; PMID:1840677

A:Accession: S22598

A:Status: Preliminary

A:Molecule type: DNA

A:Residues: 1-149 <SAM>

A:Cross-references: EMBL:X60103; MID:g53981; PIDN:CAA42697.1; PID:g53982

R:Lenstra, J.A.; Beintema, J.J.

Eur. J. Biochem. 98, 399-408, 1979

A:Title: The amino acid sequence of mouse pancreatic ribonuclease.

A:Reference number: A00830; MUID:80024269; PMID:556267

A:Accession: A00830

A:Molecule type: protein

A:Residues: 26-149 <LEN>

C:Superfamily: pancreatic ribonuclease

C:Keywords: glycoprotein; hydrolase; nucleic acid digestion; pancreas

F:1-25/Domain: signal sequence #status predicted <SIG>

F:26-149/Product: pancreatic ribonuclease #status experimental <SIG>

F:37.66.144/Active site: His, Lys, His #status predicted

F:51-109,65-120,83-135,90-97/Disulfide bonds: #status predicted

F:62,87/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 19.4%; Score 116.5; DB 1; Length 149;

Best Local Similarity 29.9%; Pred. No. 0.00018;

Matches 35; Conservative 17; Mismatches 42; Indels 23; Gaps 7;

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 22, 2004, 12:02:15 ; Search time 26.161 Seconds
(without alignments)
869.271 Million cell updates/sec

Title: US-09-622-613C-19

Perfect score: 600

Sequence: 1 QNWATFOQKHINTPIICNT.....ICVKCENQYVHFAGIGRCP 110

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 777136 seqs, 206736638 residues

Total number of hits satisfying chosen parameters: 777136

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*
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3: /cgn2_6/ptodata/1/pubaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubaa/PCTUS_PUBCOMB.pep.*
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8: /cgn2_6/ptodata/1/pubaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubaa/US09A_PUBCOMB.pep.*
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11: /cgn2_6/ptodata/1/pubaa/US09C_PUBCOMB.pep.*
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14: /cgn2_6/ptodata/1/pubaa/US10B_PUBCOMB.pep.*
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17: /cgn2_6/ptodata/1/pubaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	600	100.0	110	11	US-09-961-400-19
2	600	100.0	111	11	US-09-948-391A-21
3	600	100.0	111	11	US-09-961-400-21
4	600	100.0	117	11	US-09-948-391A-22
5	600	100.0	117	11	US-09-961-400-22
6	596	99.3	110	11	US-09-948-391A-15
7	596	99.3	110	11	US-09-961-400-15
8	596	99.3	111	11	US-09-961-400-17
9	594	99.0	110	11	US-09-948-391A-19
10	591	98.5	110	11	US-09-948-391A-24
11	591	98.5	110	11	US-09-961-400-24
12	591	98.5	111	11	US-09-948-391A-26
13	591	98.5	111	11	US-09-961-400-26
14	590	98.3	111	11	US-09-948-391A-17
15	279.5	46.6	111	11	US-09-961-400-9

16	277.5	46.2	104	11	US-09-961-400-2	Sequence 2, Appli
17	277.5	46.2	105	11	US-09-948-391A-6	Sequence 6, Appli
18	277.5	46.2	105	11	US-09-961-400-6	Sequence 6, Appli
19	277.5	46.2	127	11	US-09-948-391A-28	Sequence 28, Appli
20	277.5	46.2	127	11	US-09-961-400-28	Sequence 28, Appli
21	276.5	46.1	104	11	US-09-948-391A-2	Sequence 2, Appli
22	276.5	46.1	104	11	US-09-948-391A-4	Sequence 4, Appli
23	276.5	46.1	104	11	US-09-961-400-4	Sequence 4, Appli
24	276.5	46.1	105	11	US-09-961-400-8	Sequence 8, Appli
25	273.5	45.6	105	15	US-10-153-882-2	Sequence 2, Appli
26	272.5	45.4	104	11	US-09-948-391A-11	Sequence 11, Appli
27	272.5	45.4	104	11	US-09-961-400-11	Sequence 11, Appli
28	272.5	45.4	105	11	US-09-948-391A-13	Sequence 13, Appli
29	272.5	45.4	105	11	US-09-961-400-13	Sequence 13, Appli
30	268.5	44.8	104	11	US-09-986-119-1	Sequence 1, Appli
31	268.5	44.8	104	11	US-09-918-887-1	Sequence 1, Appli
32	267.5	44.6	105	11	US-09-948-391A-8	Sequence 8, Appli
33	267.5	44.6	111	11	US-09-948-391A-9	Sequence 9, Appli
34	202	33.7	83	10	US-09-986-119-3	Sequence 3, Appli
35	202	33.7	83	11	US-09-918-887-3	Sequence 3, Appli
36	161	26.8	169	13	US-10-016-447-2	Sequence 2, Appli
37	127.5	21.2	119	12	US-10-074-978A-139	Sequence 139, App
38	118	19.7	99	12	US-10-074-978A-141	Sequence 141, App
39	117	19.5	147	10	US-09-731-872-254	Sequence 254, App
40	117	19.5	147	12	US-09-876-997-254	Sequence 254, App
41	114	19.0	124	13	US-10-016-447-5	Sequence 5, Appli
42	113	18.8	147	9	US-09-286-240-6	Sequence 6, Appli
43	113	18.8	147	9	US-09-863-777-2	Sequence 2, Appli
44	110.5	18.4	124	10	US-09-981-286A-8	Sequence 8, Appli
45	110	18.3	131	13	US-10-016-447-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1

US-09-961-400-19
; Sequence 19, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: GOLDENBERG, DAVID M.
; APPLICANT: NEWTON, DIANNE L.
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
; TITLE OF INVENTION: CELLS
; FILE REFERENCE: 018733/1059
; CURRENT APPLICATION NUMBER: US/09/961.400
; CURRENT FILING DATE: 2001-09-25
; PRIOR FILING DATE: 09/622,613
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/079,751
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Rana catesbeiana
US-09-961-400-19

Query Match	100.0%	Score	600;	DB	11;	Length	110;
Best Local Similarity	100.0%	Pred. No.	2.9e-60;				
Matches	110;	Conservative	0;	Mismatches	0;	Indels	0;
Gaps	0;						
Qy	1	QNWATFOQKHINTPIICNTILDNNIYVGQCKRVNTFISSATTVAICTGVINLNLV	60				
Db	1	QNWATFOQKHINTPIICNTILDNNIYVGQCKRVNTFISSATTVAICTGVINLNLV	60				
Qy	61	STTRFQNTCTRTSITPRPCPSRSTETNYICVKCENQYVHFAGIGRCP	110				
Db	61	STTRFQNTCTRTSITPRPCPSRSTETNYICVKCENQYVHFAGIGRCP	110				


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; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 09/622,613
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/079,751
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Rana catesbeiana
US-09-961-400-22

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Best Local Similarity 100.0%; Pred. No. 3.1e-60;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 8 QNWATFOQKHINTPIICNTILDNNIYVGGCKRVNTFISSATTVKAICTGVINLNVL 67

Qy 61 STTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
Db 68 STTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 117

RESULT 6
US-09-948-391A-15
; Sequence 15, Application US/09948391A
; Publication No. US20030027311A1
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Recombinant Anti-Tumor RNase
; FILE REFERENCE: 015280-343110US
; CURRENT APPLICATION NUMBER: US/09/948,391A
; CURRENT FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: US 60/079,751
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: WO PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: US 09/622,613
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Rana
; OTHER INFORMATION: catesbeiana oocyte ribonuclease (RaCOR1) synthetic
; OTHER INFORMATION: gene modified to use E. coli preferred codons
US-09-948-391A-15

Query Match      99.3%; Score 596; DB 11; Length 110;
Best Local Similarity 98.2%; Pred. No. 8.1e-60;
Matches 108; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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Db 1 QNWATFOQKHINTPIICNTILDNNIYVGGCKRVNTFISSATTVKAICTGVINLNVL 60

Qy 61 STTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
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US-09-961-400-15
; Sequence 15, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: GOLDENBERG, DAVID M.
; APPLICANT: NEWTON, DIANNE L.
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
; FILE REFERENCE: 018733/1059
; CURRENT APPLICATION NUMBER: US/09/961,400
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 09/622,613
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/079,751
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Rana catesbeiana
US-09-961-400-17

Query Match      99.3%; Score 596; DB 11; Length 111;
Best Local Similarity 98.2%; Pred. No. 8.2e-60;
Matches 108; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNWATFOQKHINTPIICNTILDNNIYVGGCKRVNTFISSATTVKAICTGVINLNVL 60
Db 1 QNWATFOQKHINTPIICNTILDNNIYVGGCKRVNTFISSATTVKAICTGVINLNVL 60

Qy 61 STTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
Db 61 STTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
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RESULT 7
US-09-961-400-15
; Sequence 15, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: GOLDENBERG, DAVID M.
; APPLICANT: NEWTON, DIANNE L.
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
; FILE REFERENCE: 018733/1059
; CURRENT APPLICATION NUMBER: US/09/961,400
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 09/622,613
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/079,751
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Rana catesbeiana
US-09-961-400-15

Query Match      99.3%; Score 596; DB 11; Length 110;
Best Local Similarity 98.2%; Pred. No. 8.1e-60;
Matches 108; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QNWATFOQKHINTPIICNTILDNNIYVGGCKRVNTFISSATTVKAICTGVINLNVL 60
Db 1 QNWATFOQKHINTPIICNTILDNNIYVGGCKRVNTFISSATTVKAICTGVINLNVL 60

Qy 61 STTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
Db 61 STTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110

US-09-961-400-17
; Sequence 17, Application US/09961400
; Publication No. US20030124131A1
; GENERAL INFORMATION:
; APPLICANT: RYBAK, SUSANNA M.
; APPLICANT: GOLDENBERG, DAVID M.
; APPLICANT: NEWTON, DIANNE L.
; TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
; FILE REFERENCE: 018733/1059
; CURRENT APPLICATION NUMBER: US/09/961,400
; CURRENT FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 09/622,613
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US99/06641
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/079,751
; PRIOR FILING DATE: 1998-03-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Rana catesbeiana
US-09-961-400-17

Query Match      99.3%; Score 596; DB 11; Length 111;
Best Local Similarity 98.2%; Pred. No. 8.2e-60;
Matches 108; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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Db 1 QNWATFOQKHINTPIICNTILDNNIYVGGCKRVNTFISSATTVKAICTGVINLNVL 60

Qy 61 STTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
Db 61 STTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
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APPLICANT: as represented by The Secretary of the
APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: Recombinant Anti-Tumor RNase
FILE REFERENCE: 015280-343110US
CURRENT APPLICATION NUMBER: US/09/948,391A
CURRENT FILING DATE: 2002-05-10
PRIOR APPLICATION NUMBER: US 60/079,751
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: WO PCT/US99/06641
PRIOR FILING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: US 09/622,613
PRIOR FILING DATE: 2000-08-17
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 26
LENGTH: 111
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:Rana
OTHER INFORMATION: catesbelana ribonuclease with Met at position 1
OTHER INFORMATION: and GlnSer substitution (Met(-1) RacOR1 Q1S)
US-09-948-391A-26

Query Match 98.5%; Score 591; DB 11; Length 111;
Best Local Similarity 98.2%; Pred. No. 3e-59;
Matches 107; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 2 NWATFOQKHIIINTPIICNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVINLNVLS 61
Db 3 NWATFOQKHIIINTPIICNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVINLNVLS 62
Qy 62 TTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
Db 63 TTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111

RESULT 13
US-09-961-400-26
Sequence 26, Application US/09961400
Publication No. US20030124131A1
GENERAL INFORMATION:
APPLICANT: RYBAK, SUSANNA M.
APPLICANT: GOLDENBERG, DAVID M.
APPLICANT: NEWTON, DIANNE L.
TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
TITLE OF INVENTION: CELLS
FILE REFERENCE: 018733/1059
CURRENT APPLICATION NUMBER: US/09/961,400
CURRENT FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: 09/622,613
PRIOR FILING DATE: 2000-08-17
PRIOR APPLICATION NUMBER: PCT/US99/06641
PRIOR FILING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: 60/079,751
PRIOR FILING DATE: 1998-03-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 26
LENGTH: 111
TYPE: PRT
ORGANISM: Rana catesbelana
US-09-961-400-26

Query Match 98.5%; Score 591; DB 11; Length 111;
Best Local Similarity 98.2%; Pred. No. 3e-59;
Matches 107; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 2 NWATFOQKHIIINTPIICNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVINLNVLS 61
Db 3 NWATFOQKHIIINTPIICNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVINLNVLS 62
Qy 62 TTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110

Db 63 TTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111

RESULT 14
US-09-948-391A-17
Sequence 17, Application US/09948391A
Publication No. US20030027311A1
GENERAL INFORMATION:
APPLICANT: Rybak, Susanna M.
APPLICANT: Newton, Dianne L.
APPLICANT: The United States of America
APPLICANT: as represented by The Secretary of the
APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: Recombinant Anti-Tumor RNase
FILE REFERENCE: 015280-343110US
CURRENT APPLICATION NUMBER: US/09/948,391A
CURRENT FILING DATE: 2002-05-10
PRIOR APPLICATION NUMBER: US 60/079,751
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: WO PCT/US99/06641
PRIOR FILING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: US 09/622,613
PRIOR FILING DATE: 2000-08-17
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 17
LENGTH: 111
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:Rana
OTHER INFORMATION: catesbelana ribonuclease with Met at position 1
OTHER INFORMATION: (recombinant Met(-1) RacOR1)
US-09-948-391A-17

Query Match 98.3%; Score 590; DB 11; Length 111;
Best Local Similarity 97.3%; Pred. No. 3.9e-59;
Matches 107; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Qy 1 QNWATFOQKHIIINTPIICNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVINLNVL 60
Db 2 QNWATFOQKHIIINTPIICNTILDNNIYVGGQCKRVNTFISSATTVKAICTGVINLNVL 61
Qy 61 STTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
Db 62 STTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111

RESULT 15
US-09-961-400-9
Sequence 9, Application US/09961400
Publication No. US20030124131A1
GENERAL INFORMATION:
APPLICANT: RYBAK, SUSANNA M.
APPLICANT: GOLDENBERG, DAVID M.
APPLICANT: NEWTON, DIANNE L.
TITLE OF INVENTION: IMMUNOCONJUGATES OF TOXINS DIRECTED AGAINST MALIGNANT
TITLE OF INVENTION: CELLS
FILE REFERENCE: 018733/1059
CURRENT APPLICATION NUMBER: US/09/961,400
CURRENT FILING DATE: 2001-09-25
PRIOR APPLICATION NUMBER: 09/622,613
PRIOR FILING DATE: 2000-08-17
PRIOR APPLICATION NUMBER: PCT/US99/06641
PRIOR FILING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: 60/079,751
PRIOR FILING DATE: 1998-03-26
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 9
LENGTH: 111
TYPE: PRT
US-09-961-400-9

Search completed: January 22, 2004, 12:12:26
Job time : 26.161 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 22, 2004, 12:01:30 : Search time 13.1835 Seconds
(without alignments)
353.031 Million cell updates/sec

Title: US-09-622-613C-19
Perfect score: 600
Sequence: 1 QNWATFOQKHINTPIICNT.....ICVKCENQYVHFAGIGRCP 110

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	582.5	97.1	111	2	US-08-891-848-12
2	582.5	97.1	111	3	US-08-875-811-8
3	280.5	46.8	104	1	US-08-467-955-2
4	273.5	45.6	104	3	US-09-394-268-1
5	273.5	45.6	104	3	US-09-394-268-2
6	273.5	45.6	104	4	US-09-687-748-1
7	273.5	45.6	104	4	US-09-687-748-2
8	273.5	45.6	129	3	US-08-875-811-63
9	273.5	45.6	379	3	US-08-875-811-43
10	270.5	45.1	104	1	US-08-283-971-1
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13	270.5	45.1	104	2	US-08-891-848-13
14	270.5	45.1	105	3	US-08-875-811-39
15	270.5	45.1	355	3	US-08-875-811-41
16	270.5	45.1	358	3	US-08-875-811-51
17	268.5	44.8	104	3	US-08-875-811-1
18	268.5	44.8	104	4	US-09-071-672-1
19	268.5	44.8	106	3	US-08-875-811-28
20	268.5	44.8	107	3	US-08-875-811-30
21	268.5	44.8	112	3	US-08-875-811-32
22	268.5	44.8	251	3	US-08-875-811-59
23	268.5	44.8	254	3	US-08-875-811-61
24	268.5	44.8	355	3	US-08-875-811-49
25	268.5	44.8	355	3	US-08-875-811-57
26	268.5	44.8	355	3	US-08-875-811-64
27	268.5	44.8	366	3	US-08-875-811-55

28	263.5	43.9	105	3	US-08-875-811-24	Sequence 24, Appl
29	263.5	43.9	105	3	US-08-875-811-26	Sequence 26, Appl
30	259.5	43.2	358	3	US-08-875-811-45	Sequence 45, Appl
31	259.5	43.2	365	3	US-08-875-811-53	Sequence 53, Appl
32	245.5	40.9	107	3	US-08-875-811-20	Sequence 20, Appl
33	235.5	39.2	111	3	US-08-875-811-22	Sequence 22, Appl
34	232	38.7	114	3	US-09-223-118-3	Sequence 3, Appl
35	223.5	37.2	360	3	US-08-875-811-47	Sequence 47, Appl
36	223	37.2	114	3	US-09-223-118-2	Sequence 2, Appl
37	222	37.0	114	3	US-09-223-118-1	Sequence 1, Appl
38	221	36.8	114	3	US-09-223-118-4	Sequence 4, Appl
39	202	33.7	83	3	US-08-875-811-2	Sequence 2, Appl
40	202	33.7	83	4	US-09-071-672-3	Sequence 3, Appl
41	161	26.8	169	1	US-08-441-629-2	Sequence 2, Appl
42	161	26.8	169	3	US-08-776-207-2	Sequence 2, Appl
43	161	26.8	169	4	US-09-507-773-2	Sequence 2, Appl
44	161	26.8	169	5	PCT-US95-09172-2	Sequence 2, Appl
45	123.5	20.6	125	6	5171845-2	Patent No. 5171845

ALIGNMENTS

RESULT 1
US-08-891-848-12
: Sequence 12, Application US/08891848
: Patent No. 5955073
: GENERAL INFORMATION:
: APPLICANT: Rybak, Susanna M.
: APPLICANT: Youle, Richard J.
: APPLICANT: Newton, Dianne L.
: APPLICANT: Nicholls, Peter J.
: TITLE OF INVENTION: Selective RNase Cytotoxic Reagents
: NUMBER OF SEQUENCES: 19
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Townsend and Townsend and Crew LLP
: STREET: Two Embarcadero Center, Eighth Floor
: CITY: San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/891,848
FILING DATE: No. 5955073 yet assigned
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/125,462
FILING DATE: 22-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/014,082
FILING DATE: 04-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/779,195
FILING DATE: 22-OCT-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/510,696
FILING DATE: 20-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 015280-110110US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 111 amino acids
TYPE: amino acid

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; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..111
; OTHER INFORMATION: /note= "Frog Lectin from Rana
; OTHER INFORMATION: catesbeiana"
US-08-891-848-12

Query Match 97.1%; Score 582.5; DB 2; Length 111;
Best Local Similarity 96.4%; Pred. No. 4.9e-60;
Matches 107; Conservative 3; Mismatches 0; Indels 1; Gaps 1;

QY 1 QNWATFOOKHIINTPII-CNTILDNNIYVGGCKRVNTFISSATTVKAICTGVINLNV 59
Db 1 ENWATFOOKHIINTPIINCNTIMDNNIYVGGCKRVNTFISSATTVKAICTGVINMV 60

QY 60 LSTTRFQLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
Db 61 LSTTRFQLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111

RESULT 2
US-08-875-811-8
; Sequence 8, Application US/08875811
; Patent No. 6045791
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Boque, Lluís
; APPLICANT: Wlodawer, Alexander
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,811
; FILING DATE: 19-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/02588
; FILING DATE: 19-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/011,800
; FILING DATE: 21-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Paris, Susan K.
; REGISTRATION NUMBER: 41,739
; REFERENCE/DOCKET NUMBER: 015280-244100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 111 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..111

; OTHER INFORMATION: /note= "Frog Lectin from Rana
; OTHER INFORMATION: catesbeiana"
US-08-875-811-8

Query Match 97.1%; Score 582.5; DB 3; Length 111;
Best Local Similarity 96.4%; Pred. No. 4.9e-60;
Matches 107; Conservative 3; Mismatches 0; Indels 1; Gaps 1;

QY 1 QNWATFOOKHIINTPII-CNTILDNNIYVGGCKRVNTFISSATTVKAICTGVINLNV 59
Db 1 ENWATFOOKHIINTPIINCNTIMDNNIYVGGCKRVNTFISSATTVKAICTGVINMV 60

QY 60 LSTTRFQLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
Db 61 LSTTRFQLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111

RESULT 3
US-08-467-955-2
; Sequence 2, Application US/08467955
; Patent No. 5728805
; GENERAL INFORMATION:
; APPLICANT: Ardelt Ph.D, Wojciech J.
; TITLE OF INVENTION: PHARMACEUTICALS AND METHOD FOR MAKING THEM
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Mark H. Jay, P.A.
; STREET: P.O. Box E
; CITY: Short Hills
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07078-0383
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,955
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/178,118
; FILING DATE: 06-APR-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/436,141
; FILING DATE: 13-NOV-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/814,332
; FILING DATE: 03-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/283,970
; FILING DATE: 01-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Jay, Mark H.
; REGISTRATION NUMBER: 27507
; REFERENCE/DOCKET NUMBER: 5007 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-912-9066
; TELEFAX: 201-912-0442
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 104 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: N
; ANTI-SENSE: N
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Rana pipiens
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/283,971
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/921,180
; FILING DATE: 30-JUL-1992
; APPLICATION NUMBER: US 07/178,118
; FILING DATE: 06-APR-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/436,141
; FILING DATE: 13-NOV-1989
; REFERENCE/DOCKET NUMBER: 27507
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 718-625-0399
; TELEFAX: 718-625-0399
; NAME: Jay, Mark H.
; ATTORNEY/AGENT INFORMATION:
; REGISTRATION NUMBER: 27507
; REFERENCE/DOCKET NUMBER: 5006 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 718-625-0399
; TELEFAX: 718-625-0399
; TELEX: No. 5529775 Applicable
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 104 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: N
; ANTI-SENSE: N
; FRAGMENT TYPE: N-terminal
; ORGANISM: Rana pipiens
; DEVELOPMENTAL STAGE: Embryo
;
; US-08-283-971-1
;
; Query Match 45.1%; Score 270.5; DB 1; Length 104;
; Best Local Similarity 47.7%; Pred. No. 5.2e-24;
; Matches 53; Conservative 17; Mismatches 33; Indels 9; Gaps 4;
;
; QY 1 QNWATFOQKHINT-PIICNTILDNNIYVGGQKRVNTFISSATTVAICTGVI-NLN 58
; Db 1 EDWLTFOQKHITNRDVCNIMSTNLF---HCKDKNTFIYSRPEPVKAICKGIIASKN 56
;
; QY 59 VLSITRFLQNTCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRC 109
; Db 57 VLTTFSEFYLSDC---NVTSRPKYKXKSTNKFCTVCENQAPVHFVGVGSC 104
;
; RESULT 11
; US-07-921-619-1
; Sequence 1, Application US/07921619
; Patent No. 5595734
; GENERAL INFORMATION:
; APPLICANT: Ardeit Ph.D, Wojciech J.
; TITLE OF INVENTION: Mikulski, Stanislaw M.
; TITLE OF INVENTION: PHARMACEUTICAL FOR TREATING TUMORS IN HUMANS
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Mark H. Jay, P.C.
; STREET: P.O. Box 020083, General Post Office
; CITY: Brooklyn
; STATE: New York
; COUNTRY: USA
; ZIP: 11202-0002
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
;
; US-08-283-971-1
; Query Match 45.1%; Score 270.5; DB 1; Length 104;
; Best Local Similarity 47.7%; Pred. No. 5.2e-24;
; Matches 53; Conservative 17; Mismatches 33; Indels 9; Gaps 4;
;
; QY 1 QNWATFOQKHINT-PIICNTILDNNIYVGGQKRVNTFISSATTVAICTGVI-NLN 58
; Db 1 EDWLTFOQKHITNRDVCNIMSTNLF---HCKDKNTFIYSRPEPVKAICKGIIASKN 56
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; QY 59 VLSITRFLQNTCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRC 109
; Db 57 VLTTFSEFYLSDC---NVTSRPKYKXKSTNKFCTVCENQAPVHFVGVGSC 104
;
; RESULT 12
; US-08-467-955-1
; Sequence 1, Application US/08467955
; Patent No. 5728805
; GENERAL INFORMATION:
; APPLICANT: Ardeit Ph.D, Wojciech J.
; TITLE OF INVENTION: PHARMACEUTICALS AND METHOD FOR MAKING THEM
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Mark H. Jay, P.A.
; STREET: P.O. Box E
; CITY: Short Hills
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07078-0383
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,955
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/178,118
; FILING DATE: 06-APR-1988
; CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US 07/436,141
; FILING DATE: 13-NOV-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/814,332
; FILING DATE: 03-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/283,970
; FILING DATE: 01-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Jay, Mark H.
; REGISTRATION NUMBER: 27507
; REFERENCE/DOCKET NUMBER: 5007 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-912-9066
; TELEFAX: 201-912-0442
; TELEX: No. 572805 Applicable
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 104 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: N
; ANTI-SENSE: N
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Rana pipiens
; DEVELOPMENTAL STAGE: Oocyte
; US-08-467-955-1

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Query Match 45.1%; Score 270.5; DB 1; Length 104;
Best Local Similarity 47.7%; Pred. No. 5.2e-24;
Matches 53; Conservative 17; Mismatches 32; Indels 9; Gaps 4;

Qy 1 QNWATFOQRHIIT-PIICNTILDNNIYVGGCKRVNTFISSATTVKAICTGVI-NLN 58
Db 1 EDMLTFQKHITNTRDVCNDIMSTNLF---HCKDKNTFIYSRPPVKAICKGIASKN 56

Qy 59 VLSTTRFQNLCTRTSITRPPCPYSSRTETNYICVKCENQYVHFAGIGRC 109
Db 57 VLTTSFYLSDC---NVTSRPCKYKLKSTNKFVCVTENQAPVHFVGVGSC 104

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RESULT 13
US-08-891-848-13
; Sequence 13, Application US/08891848
; Patent No. 5955073
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Youle, Richard J.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Nicholls, Peter J.
; TITLE OF INVENTION: Selective RNase Cytotoxic Reagents
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/891,848
; FILING DATE: No. 5955073 yet assigned
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/125,462

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; FILING DATE: 22-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/014,082
; FILING DATE: 04-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/779,195
; FILING DATE: 22-OCT-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/510,696
; FILING DATE: 20-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 015280-110310US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 104 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
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; OTHER INFORMATION: /label= Onc
; OTHER INFORMATION: /note= "Oncanase from Rana pipiens"
; US-08-891-848-13

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Query Match 45.1%; Score 270.5; DB 2; Length 104;
Best Local Similarity 47.7%; Pred. No. 5.2e-24;
Matches 53; Conservative 17; Mismatches 32; Indels 9; Gaps 4;

Qy 1 QNWATFOQRHIIT-PIICNTILDNNIYVGGCKRVNTFISSATTVKAICTGVI-NLN 58
Db 1 EDMLTFQKHITNTRDVCNDIMSTNLF---HCKDKNTFIYSRPPVKAICKGIASKN 56

Qy 59 VLSTTRFQNLCTRTSITRPPCPYSSRTETNYICVKCENQYVHFAGIGRC 109
Db 57 VLTTSFYLSDC---NVTSRPCKYKLKSTNKFVCVTENQAPVHFVGVGSC 104

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RESULT 14
US-08-875-811-39
; Sequence 39, Application US/08875811
; Patent No. 6045793
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Boque, Lluis
; APPLICANT: Wlodawer, Alexander
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,811
; FILING DATE: 19-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/02588

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; FILING DATE: 19-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/011,800
; FILING DATE: 21-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Paris, Susan K.
; REGISTRATION NUMBER: 41,739
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 105 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-875-811-39

Query Match 45.1%; Score 270.5; DB 3; Length 105;
Best Local Similarity 47.7%; Pred. No. 5.3e-24;
Matches 53; Conservative 17; Mismatches 33; Indels 9; Gaps 4;

Qy 1 QNWATFOQKHINT-PIICNTILDNNIYVGGQCKRVNTFIISATTVAICTGVI-NLN 58
Db 2 EDWLTFOKKHITNTRDVCNDIMSTNLF---HCKDKNTFIYSRPEPVKAICKGIIASKN 57

Qy 59 VLSTTRFQLNCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRC 109
Db 58 VLTTSEFYLSDC---NVTSRPKYKLLKSTNKFVCVTENQAPVHFVGVGSC 105

RESULT 15
US-08-875-811-41
; Sequence 41, Application US/08875811
; Patent No. 6045793
; GENERAL INFORMATION:
; APPLICANT: Rybak, Susanna M.
; APPLICANT: Newton, Dianne L.
; APPLICANT: Boque, Lluís
; APPLICANT: Wlodawer, Alexander
; TITLE OF INVENTION: Recombinant Ribonuclease Proteins
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,811
; FILING DATE: 19-FEB-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US97/02588
; FILING DATE: 19-FEB-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/011,800
; FILING DATE: 21-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Paris, Susan K.
; REGISTRATION NUMBER: 41,739
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 41:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-875-811-41

Query Match 45.1%; Score 270.5; DB 3; Length 355;
Best Local Similarity 47.7%; Pred. No. 2.3e-23;
Matches 53; Conservative 17; Mismatches 32; Indels 9; Gaps 4;

Qy 1 QNWATFOQKHINT-PIICNTILDNNIYVGGQCKRVNTFIISATTVAICTGVI-NLN 58
Db 252 EDWLTFOKKHITNTRDVCNDIMSTNLF---HCKDKNTFIYSRPEPVKAICKGIIASKN 307

Qy 59 VLSTTRFQLNCTRTSITPRPCPYSSRTETNYICVKCENQYVHFAGIGRC 109
Db 308 VLTTSEFYLSDC---NVTSRPKYKLLKSTNKFVCVTENQAPVHFVGVGSC 355

Search completed: January 22, 2004, 12:10:07
Job time : 13.1835 secs

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OM protein - protein search, using sw model

Run on: January 22, 2004, 12:01:20 ; Search time 34.6067 Seconds
(without alignments)
504.524 Million cell updates/sec

Title: US-09-622-613C-19

Perfect score: 600

Sequence: 1 QNWATFQKHIIINTPIICNT.....ICVKENQYVHPFAGIGRCP 110

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
3: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
4: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
5: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
6: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
7: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
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14: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1993.DAT.*
15: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
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17: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.*
18: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
19: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
20: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
21: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	600	100.0	110	20	Recombinant RacOR1
2	600	100.0	111	20	Recombinant Met(-1
3	596	99.3	110	20	Rana catesbeiana o
4	596	99.3	111	20	Recombinant Met(-1
5	591	98.5	110	20	Recombinant RacOR1
6	591	98.5	111	20	Recombinant Met(-1
7	582.5	97.1	111	20	Frog lectin protein
8	280.5	46.8	104	18	Antitumour protein
9	279.5	46.6	104	20	Recombinant RaPLR1

10	279.5	46.6	105	20	AAV28869	Recombinant Met(-1
11	277.5	46.2	104	20	AAV28865	Rana pipiens liver
12	277.5	46.2	105	20	AAV28867	Recombinant Met(-1
13	277.5	46.2	127	20	AAV28879	Rana pipiens Clone
14	273.5	45.6	104	18	AAW30301	Recombinant onc pr
15	273.5	45.6	104	22	AAW31666	Amino acid sequenc
16	273.5	45.6	104	22	AAW31667	Amino acid sequenc
17	273.5	45.6	104	23	ABG31617	Northern leopard f
18	273.5	45.6	104	23	ABG32650	Northern leopard f
19	273.5	45.6	105	20	AAV39400	Recombinant frog O
20	273.5	45.6	379	18	AAW35126	R. pipiens recombi
21	272.5	45.4	104	18	AAW30302	Recombinant onc pr
22	272.5	45.4	104	20	AAV28870	Recombinant RaPLR1
23	272.5	45.4	105	20	AAV28871	Recombinant Met(-1
24	270.5	45.1	104	12	AAW12344	Protein with activ
25	270.5	45.1	104	15	AAW47303	ONCONASE (pharmac
26	270.5	45.1	104	17	AAW00736	Protein derived fr
27	270.5	45.1	104	18	AAW06543	Antitumour protein
28	270.5	45.1	104	18	AAW14065	Onconase (RTM) pro
29	270.5	45.1	104	20	AAV33322	Onconase (RTM) pro
30	270.5	45.1	104	20	AAW88233	Frog onconase prot
31	270.5	45.1	105	18	AAW35123	R. pipiens recombi
32	270.5	45.1	355	18	AAW35125	R. pipiens recombi
33	270.5	45.1	358	18	AAW35130	R. pipiens recombi
34	268.5	44.8	106	18	AAW35122	R. pipiens recombi
35	268.5	44.8	107	18	AAW35117	R. pipiens recombi
36	268.5	44.8	112	18	AAW35118	R. pipiens recombi
37	268.5	44.8	251	18	AAW35134	R. pipiens recombi
38	268.5	44.8	254	18	AAW35135	R. pipiens recombi
39	268.5	44.8	355	18	AAW35129	R. pipiens recombi
40	268.5	44.8	355	18	AAW35133	R. pipiens recombi
41	268.5	44.8	366	18	AAW35132	R. pipiens recombi
42	263.5	43.9	104	18	AAW18224	Antitumour generi
43	263.5	43.9	105	18	AAW35115	R. pipiens recombi
44	263.5	43.9	105	18	AAW35116	R. pipiens recombi
45	259.5	43.2	358	18	AAW35127	R. pipiens recombi

ALIGNMENTS

RESULT 1
AAV28874
ID AAY28874 standard; Protein; 110 AA.

XX AAY28874;

AC AAY28874;

XX 25-JAN-2000 (first entry)

DT 25-JAN-2000 (first entry)

XX Recombinant RacOR1 Met22Leu Met57Leu amino acid sequence.

DE Recombinant RacOR1 Met22Leu Met57Leu amino acid sequence.

XX Recombinant Rana catesbeiana oocyte ribonuclease; covalently bound;

KW RacOR1 Met22Leu Met57Leu; LL2 antibody; ligand binding moiety; CD22;

KW cancerous B cell; Kaposi's sarcoma; human chorionic gonadotropin; hCG;

KW signal peptide; recombinant ribonuclease; cytotoxic fusion protein;

KW cancer; bullfrog; RNase; autoimmune disease.

XX Rana catesbeiana.

OS Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 22 /note= "Wild type Met replaced with Leu"

FT Misc-difference 57 /note= "Wild type Met replaced with Leu"

FT Misc-difference 57 /note= "Wild type Met replaced with Leu"

XX W09950398-A2.

PN 07-OCT-1999.

PD 26-MAR-1999;

XX 99WO-US06641.

XX 27-MAR-1998;

PR 98US-0079751.

XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX PI Newton DL, Rybak SM;
 XX XX WPI; 1999-610847/52.
 DR N-PSDB; AAZ08132.
 XX XX
 PT New recombinant ribonucleases, used for killing target cells, e.g. for
 PT treating cancers, viral infections or autoimmune diseases -
 XX PS Claim 22; Page 64; 71pp; English.
 XX XX
 CC The present sequence is a recombinant Rana catesbeiana oocyte
 CC ribonuclease (RaCOR1) protein with Met22Leu Met57Leu. Carboxy terminal
 CC end of recombinant RaCOR1 has a covalently bound ligand binding moiety,
 CC which can be a LL2 antibody directed against CD22 on cancerous B cells
 CC or human chorionic gonadotrophin (hCG) effective against Kaposi's sarcoma
 CC cells. Recombinant ribonucleases can be expressed in bacteria without an
 CC N-terminal methionine due to the presence of a signal peptide that is
 CC cleaved by bacteria. The soluble expression of ribonuclease allows the
 CC proteins to be fused in-frame with ligand binding moieties to form
 CC cytotoxic fusion proteins. They can be used for treatment of cancer and
 CC autoimmune diseases.
 XX XX
 SQ Sequence 110 AA;
 Query Match 100.0%; Score 600; DB 20; Length 110;
 Best Local Similarity 100.0%; Pred. No. 6.1e-60;
 Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QNWATFOQKHINTPIICNTILDNNIYVGGQCKRVNTFIISATTVKAICTGVINLNL 60
 DB 1 QNWATFOQKHINTPIICNTILDNNIYVGGQCKRVNTFIISATTVKAICTGVINLNL 60
 QY 61 STTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
 DB 61 STTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
 RESULT 2
 AAY28876
 ID AAY28876 standard; Protein; 111 AA.
 XX AC AAY28876;
 XX DT 25-JAN-2000 (first entry)
 XX DE Recombinant Met(-1) RaCOR1 Met22Leu Met57Leu-(His)6 protein.
 XX KW Met(-1) Rana catesbeiana ribonuclease Met22Leu Met57Leu-(His)6; RaCOR1;
 KW recombinant; CD22; covalently bound; LL2 antibody; ligand binding moiety;
 KW cancerous B cell; Kaposi's sarcoma; human chorionic gonadotrophin; hCG;
 KW signal peptide; recombinant ribonuclease; cytotoxic fusion protein;
 KW cancer; bullfrog; RNase; autoimmune disease.
 XX OS Rana catesbeiana.
 XX OS Synthetic.
 FH Key Location/Qualifiers
 FT Misc-difference 1 /note= "(His)6 histidine tag attached to N-terminal Met"
 FT Misc-difference 1 /note= "Met not found in wild type RaCOR1"
 FT Misc-difference 23 /note= "Wild type Met replaced with Leu"
 FT Misc-difference 58 /note= "Wild type Met replaced with Leu"
 FT XX
 XX PN WO9950398-A2.
 XX XX 07-OCT-1999.
 XX PD
 XX XX

PP 26-MAR-1999; 99WO-US06641.
 XX PR 27-MAR-1998; 98US-0079751.
 XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX PI Newton DL, Rybak SM;
 XX XX WPI; 1999-610847/52.
 DR N-PSDB; AAZ08133.
 XX XX
 PT New recombinant ribonucleases, used for killing target cells, e.g. for
 PT treating cancers, viral infections or autoimmune diseases -
 XX PS Claim 22; Page 66; 71pp; English.
 XX XX
 CC The present sequence is a recombinant Rana catesbeiana oocyte
 CC ribonuclease (RaCOR1) protein with Met at position 1 attached to a
 CC (His)6 tag, Met23Leu and Met58Leu. Carboxy terminal end of recombinant
 CC RaCOR1 has a covalently bound ligand binding moiety, which can be a LL2
 CC antibody directed against CD22 on cancerous B cells or human chorionic
 CC gonadotrophin (hCG) effective against Kaposi's sarcoma cells. Recombinant
 CC ribonucleases can be expressed in bacteria without an N-terminal
 CC methionine due to the presence of a signal peptide that is cleaved by
 CC bacteria. The soluble expression of ribonuclease allows the proteins to
 CC be fused in-frame with ligand binding moieties to form cytotoxic fusion
 CC proteins. They can be used for treatment of cancer and autoimmune
 CC diseases.
 XX XX
 SQ Sequence 111 AA;
 Query Match 100.0%; Score 600; DB 20; Length 111;
 Best Local Similarity 100.0%; Pred. No. 6.2e-60;
 Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QNWATFOQKHINTPIICNTILDNNIYVGGQCKRVNTFIISATTVKAICTGVINLNL 60
 DB 2 QNWATFOQKHINTPIICNTILDNNIYVGGQCKRVNTFIISATTVKAICTGVINLNL 61
 QY 61 STTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
 DB 62 STTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
 RESULT 3
 AAY28872
 ID AAY28872 standard; Protein; 110 AA.
 XX AC AAY28872;
 XX DT 25-JAN-2000 (first entry)
 XX DE Rana catesbeiana oocyte ribonuclease (RaCOR1) amino acid sequence.
 XX KW Rana catesbeiana oocyte ribonuclease; RaCOR1; covalently bound; CD22;
 KW LL2 antibody; ligand binding moiety; cancerous B cell; Kaposi's Sarcoma;
 KW human chorionic gonadotrophin; hCG; recombinant ribonuclease; bullfrog;
 KW signal peptide; cytotoxic fusion protein; cancer; autoimmune disease;
 KW RNase.
 XX OS Rana catesbeiana.
 XX OS Synthetic.
 XX PN WO9950398-A2.
 XX PD 07-OCT-1999.
 XX PF 26-MAR-1999; 99WO-US06641.
 XX PR 27-MAR-1998; 98US-0079751.
 XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX XX

PI Newton DL, Rybak SM;
 XX WPI; 1999-610847/52.
 DR N-PSDB; AAZ08130.
 XX
 PT New recombinant ribonucleases, used for killing target cells, e.g. for
 PT treating cancers, viral infections or autoimmune diseases -
 XX
 PS Claim 22; Page 62; 71pp; English.
 XX
 CC The present sequence is a Rana catesbeiana oocyte ribonuclease (RaCOR1)
 CC protein encoded by a cDNA modified for expression in E. coli. Carboxy
 CC terminal end of RaCOR1 has a covalently bound ligand binding moiety,
 CC which can be a LL2 antibody directed against CD22 on cancerous B cells
 CC or human chorionic gonadotropin (hCG) effective against Kaposi's
 CC Sarcoma cells. Recombinant ribonucleases can be expressed in bacteria
 CC without an N-terminal methionine due to the presence of a signal peptide
 CC that is cleaved by bacteria. The soluble expression of ribonuclease
 CC allows the proteins to be fused in-frame with ligand binding moieties to
 CC form cytotoxic fusion proteins. They can be used for treatment of cancer
 CC and autoimmune diseases.
 XX
 SQ Sequence 110 AA;
 Query Match 99.3%; Score 596; DB 20; Length 110;
 Best Local Similarity 98.2%; Pred. No. 1.7e-59;
 Matches 108; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QNWATFOOKHIINTPIICNTILDNNIYVGQCKRVNTFISSATTVKAICTGVINLNL 60
 DB 1 QNWATFOOKHIINTPIICNTIMDNNIYVGQCKRVNTFISSATTVKAICTGVINLNL 60
 QY 61 STTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
 DB 61 STTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
 RESULT 4
 AAY28873
 ID AAY28873 standard; Protein; 111 AA.
 AC AAY28873;
 XX
 DT 25-JAN-2000 (first entry)
 DE Recombinant Met(-1) RaCOR1.
 KW Recombinant Met(-1) Rana catesbeiana oocyte ribonuclease; RaCOR1; CD22;
 KW covalently bound; LL2 antibody; ligand binding moiety; cancerous B cell;
 KW Kaposi's sarcoma; human chorionic gonadotropin; hCG; signal peptide;
 KW recombinant ribonuclease; cytotoxic fusion protein; cancer; bullfrog;
 KW RNase; autoimmune disease.
 XX
 OS Rana catesbeiana.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1 /note= "Met not found in wild type RaCOR1"
 FT
 XX WO9950398-A2.
 XX
 PD 07-OCT-1999.
 XX
 XX 26-MAR-1999; 99WO-US06641.
 XX
 XX 27-MAR-1998; 98US-0079751.
 XX
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 XX Newton DL, Rybak SM;
 XX WPI; 1999-610847/52.
 XX
 XX WPI; 1999-610847/52.

DR N-PSDB; AAZ08131.
 XX
 PT New recombinant ribonucleases, used for killing target cells, e.g. for
 PT treating cancers, viral infections or autoimmune diseases -
 XX
 PS Claim 22; Page 63; 71pp; English.
 XX
 CC The present sequence is a recombinant Rana catesbeiana oocyte
 CC ribonuclease (RaCOR1) protein with Met at position 1. Carboxy terminal
 CC end of recombinant RaCOR1 has a covalently bound ligand binding moiety,
 CC which can be a LL2 antibody directed against CD22 on cancerous B cells or
 CC human chorionic gonadotropin (hCG) effective against Kaposi's sarcoma
 CC cells. Recombinant ribonucleases can be expressed in bacteria without an
 CC N-terminal methionine due to the presence of a signal peptide that is
 CC cleaved by bacteria. The soluble expression of ribonuclease allows the
 CC proteins to be fused in-frame with ligand binding moieties to form
 CC cytotoxic fusion proteins. They can be used for treatment of cancer and
 CC autoimmune diseases.
 XX
 SQ Sequence 111 AA;
 Query Match 99.3%; Score 596; DB 20; Length 111;
 Best Local Similarity 98.2%; Pred. No. 1.8e-59;
 Matches 108; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 QNWATFOOKHIINTPIICNTILDNNIYVGQCKRVNTFISSATTVKAICTGVINLNL 60
 DB 2 QNWATFOOKHIINTPIICNTIMDNNIYVGQCKRVNTFISSATTVKAICTGVINLNL 61
 QY 61 STTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
 DB 62 STTRFQNTCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111
 RESULT 5
 AAY28877
 ID AAY28877 standard; Protein; 110 AA.
 AC AAY28877;
 XX
 DT 25-JAN-2000 (first entry)
 DE Recombinant RaCOR1 Gln1Ser amino acid sequence.
 KW Recombinant Rana catesbeiana oocyte ribonuclease; RaCOR1 Gln1Ser; CD22;
 KW covalently bound; LL2 antibody; ligand binding moiety; cancerous B cell;
 KW bullfrog; Kaposi's sarcoma; human chorionic gonadotropin; hCG; RNase;
 KW signal peptide; recombinant ribonuclease; cytotoxic fusion protein;
 KW cancer; autoimmune disease.
 XX
 OS Rana catesbeiana.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1 /note= "Wild type Gln replaced with Ser"
 FT
 XX WO9950398-A2.
 XX
 PD 07-OCT-1999.
 XX
 XX 26-MAR-1999; 99WO-US06641.
 XX
 XX 27-MAR-1998; 98US-0079751.
 XX
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 XX Newton DL, Rybak SM;
 XX WPI; 1999-610847/52.
 XX
 XX N-PSDB; AAZ08134.
 XX
 PT New recombinant ribonucleases, used for killing target cells, e.g. for

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PT treating cancers, viral infections or autoimmune diseases
XX
PS Claim 22; Page 67; 71pp; English.
XX
CC The present sequence is a recombinant Rana catesbeiana oocyte
CC ribonuclease (RaCOR1) protein with Gln1Ser. Carboxy terminal end of
CC recombinant RaCOR1 has a covalently bound ligand binding moiety, which
CC can be a LL2 antibody directed against CD22 on cancerous B cells or
CC human chorionic gonadotrophin (hCG) effective against Kaposi's sarcoma
CC cells. Recombinant ribonucleases can be expressed in bacteria without an
CC N-terminal methionine due to the presence of a signal peptide that is
CC cleaved by bacteria. The soluble expression of ribonuclease allows the
CC proteins to be fused in-frame with ligand binding moieties to form
CC cytotoxic fusion proteins. They can be used for treatment of cancer and
CC autoimmune diseases.
XX
SQ Sequence 110 AA;
    Query Match      98.5%; Score 591; DB 20; Length 110;
    Best Local Similarity 98.2%; Pred. No. 6.4e-59;
    Matches 107; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
OY 2 NWATFOQKHINTPIICNTILDNNIYVGGQCKRVNTFIISATTVKAICTGVINLVLS 61
DB 2 NWATFOQKHINTPIICNTILDNNIYVGGQCKRVNTFIISATTVKAICTGVINLVLS 61
OY 62 TTRFQNTCTRTSITPRCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
DB 62 TTRFQNTCTRTSITPRCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110

RESULT 6
AAV28878
ID AAV28878 standard; Protein; 111 AA.
XX
AC AAV28878;
XX
DT 25-JAN-2000 (first entry)
XX
DE Recombinant Met(-1) RaCOR1 Gln1Ser amino acid sequence.
XX
KW Recombinant Met(-1) Rana catesbeiana oocyte ribonuclease Gln1Ser; RaCOR1;
KW covalently bound; LL2 antibody; ligand binding moiety; cancerous B cell;
KW Kaposi's sarcoma; human chorionic gonadotrophin; hCG; signal peptide;
KW recombinant ribonuclease; cytotoxic fusion protein; cancer; bullfrog;
KW CD22; RNase; autoimmune disease.
XX
OS Rana catesbeiana.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 1 /note= "Met not found in wild type RaCOR1"
FT Misc-difference 2 /note= "Wild type Gln replaced with Ser"
XX
PN WO950398-A2.
XX
PD 07-OCT-1999.
XX
PF 26-MAR-1999; 99WO-US06641.
XX
PR 27-MAR-1998; 98US-0079751.
XX
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Newton DL, Rybak SM;
XX
DR WPI; 1999-610847/52.
XX
DR N-PSDB; AAZ08135.
XX
PT New recombinant ribonucleases, used for killing target cells, e.g. for
PT treating cancers, viral infections or autoimmune diseases
XX

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XX Claim 22; Page 68; 71pp; English.
XX
CC The present sequence is a recombinant Rana catesbeiana ribonuclease
CC (RaCOR1) protein with Met at position 1 and Gln2Ser. Carboxy terminal end
CC of recombinant RaCOR1 has a covalently bound ligand binding moiety, which
CC can be a LL2 antibody directed against CD22 on cancerous B cells or human
CC chorionic gonadotrophin (hCG) effective against Kaposi's sarcoma cells.
CC Recombinant ribonucleases can be expressed in bacteria without an N-
CC terminal methionine due to the presence of a signal peptide that is
CC cleaved by bacteria. The soluble expression of ribonuclease allows the
CC proteins to be fused in-frame with ligand binding moieties to form
CC cytotoxic fusion proteins. They can be used for treatment of cancer and
CC autoimmune diseases.
XX
SQ Sequence 111 AA;
    Query Match      98.5%; Score 591; DB 20; Length 111;
    Best Local Similarity 98.2%; Pred. No. 6.5e-59;
    Matches 107; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
OY 2 NWATFOQKHINTPIICNTILDNNIYVGGQCKRVNTFIISATTVKAICTGVINLVLS 61
DB 3 NWATFOQKHINTPIICNTILDNNIYVGGQCKRVNTFIISATTVKAICTGVINLVLS 62
OY 62 TTRFQNTCTRTSITPRCPYSSRTETNYICVKCENQYPVHFAGIGRCP 110
DB 63 TTRFQNTCTRTSITPRCPYSSRTETNYICVKCENQYPVHFAGIGRCP 111

RESULT 7
AAV33321
ID AAV33321 standard; Protein; 111 AA.
XX
AC AAV33321;
XX
DT 29-NOV-1999 (first entry)
XX
DE Frog lectin protein fragment.
XX
KW Cytotoxic; RNase; ribonuclease; pancreatic; antibody; light chain;
KW heavy chain; cell surface marker; treatment; tumor; viral infection;
KW parasite infection; immune dysfunctional cell; autoimmune disease;
KW contraceptive; cell separation; transplantation; bone marrow ablation;
KW leukemia cell; T-cell; graft-versus-host disease; bullfrog; lectin.
XX
OS Rana catesbeiana.
XX
PN US5955073-A.
XX
PD 21-SEP-1999.
XX
PF 09-JUL-1997; 97US-0891849.
XX
PR 22-SEP-1993; 93US-0125462.
PR 22-OCT-1991; 91US-0779195.
PR 20-APR-1990; 90US-0510696.
PR 04-FEB-1993; 93US-0014082.
XX
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Rybak SM, Newton DL, Nicholls PJ, Youle RJ;
XX
DR WPI; 1999-560488/47.
XX
PT Recombinantly fused pancreatic RNase-targeting proteins useful for
PT treating tumors, infections, immune or autoimmune disorders and as a
PT contraceptive
XX
PS Example 3; Fig 19; 47pp; English.
XX
PT This invention describes a novel nucleic acid construct comprising
XX sequences encoding functional pancreatic RNase and a second protein

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The present sequence is a specifically claimed example of an antitumour protein from the generic protein in AAW18224, with the molecular weight 12000. This is one of two preferred proteins (the other in AAW0543) that have been isolated from *Rana pipiens* oocytes. Both proteins have a blocked amino terminal group and are essentially free of carbohydrates. The proteins are used to treat tumours. Use of the peptides has fewer disadvantages than chemotherapy, radiotherapy

Db 80 VLTTFEYLSDC---NVTSPCKYKXKSTNTFCVTCENQAPVHFVGVGHC 127

RESULT 14
AAW30301
ID AAW30301 standard; protein; 104 AA.
XX
AC AAW30301;
XX
DT 09-JUN-1998 (first entry)
XX
DE Recombinant onc protein.
XX
KW Onc; oncanase; ribonuclease; frog; antitumour; pancreatic cancer;
KW human immunodeficiency virus type-1; HIV1; replication.
XX
OS Rana pipiens.
XX
PN WO9738112-A1.
XX
PD 16-OCT-1997.
XX
PF 04-APR-1997; 97WO-US05675.
XX
PR 04-APR-1996; 96US-0626288.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Ardelit W, Boix E, Vasandani VM, Wu YN, Youle RJ;
XX
DR WPI; 1997-512725/47.
XX
PT Recombinant Onc protein with glutamine residue at position 1 -
PT useful as antitumour and antiviral agent, also as cell culture
PT selection agent
XX
PS Claim 1; Page 28; 35pp; English.
XX
CC This sequence represents a recombinant Onc protein comprising a 104 amino
CC acid sequence having Gln at position 1. Onc, a ribonuclease from Rana
CC pipiens oocytes, is known as an antitumour agent (e.g. for treating
CC pancreatic cancer) and inhibitor of human immunodeficiency virus type-1
CC replication. It can be used therapeutically or as a cell-culture
CC selection agent, e.g. to identify gene therapy compositions able to
CC inhibit tumour growth.
XX
SQ Sequence 104 AA;
Query Match 45.6%; Score 273.5; DB 18; Length 104;
Best Local Similarity 48.6%; Pred. No. 4.2e-23;
Matches 54; Conservative 16; Mismatches 32; Indels 9; Gaps 4;
QY 1 QNWATFOQKHINT-PIICNTILDNNIYVGGCKRVNTFISSATTVKAICTGVI-NLN 58
DB 1 QDWLTFQKHITNTRDVCNIMSTNLF---HCKDKNTFIYSRPEPVKAICKGIATSKN 56
QY 59 VLSTTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
DB 57 VLTTFEYLSDC---NVTSPCKYKXKSTNTFCVTCENQAPVHFVGVGSC 104

RESULT 15
AAB31666
ID AAB31666 standard; protein; 104 AA.
XX
AC AAB31666;
XX
DT 30-APR-2001 (first entry)
XX
DE Amino acid sequence of a frog ribonuclease protein.
XX
KW Frog; ribonuclease; ranpirnase; RNase.

OS Rana pipiens.
XX
FH Key Location/Qualifiers
FT Modified-site 1
FT /note= "this Gln is autocyclised to pyroglutamic acid"
XX
PN US6175003-B1.
XX
PD 16-JAN-2001.
XX
PF 10-SEP-1999; 99US-0394268.
XX
PR 10-SEP-1999; 99US-0394268.
XX
PA (ALFA-) ALFACELL CORP.
XX
PI Saxena SK;
XX
DR WPI; 2001-167808/17.
XX
PT New nucleic acids encoding a ribonuclease (Rnase), useful for the
PT precise targeting of Rnase to a predetermined cell receptor -
XX
PS Claim 1; Columns 5-6; 7pp; English.
XX
CC The present sequence represents a frog ribonuclease protein (ranpirnase)
CC (RNase). The specification describes a synthetic ribonuclease protein,
CC in which the addition of cysteine in the ribonuclease facilitates the
CC chemical linking of a targeting molecule by the single reactive
CC sulphydryl group. The specification also describes a method for the
CC production of ranpirnase using DNA technology instead of processing
CC biological material. The re-engineering of the protein molecule allows
CC easier attachment to a targeting molecule thereby making it possible for
CC the ribonuclease to be delivered to a particular cell receptor where it
CC might be most effective.
XX
SQ Sequence 104 AA;
Query Match 45.6%; Score 273.5; DB 22; Length 104;
Best Local Similarity 48.6%; Pred. No. 4.2e-23;
Matches 54; Conservative 16; Mismatches 32; Indels 9; Gaps 4;
QY 1 QNWATFOQKHINT-PIICNTILDNNIYVGGCKRVNTFISSATTVKAICTGVI-NLN 58
DB 1 QDWLTFQKHITNTRDVCNIMSTNLF---HCKDKNTFIYSRPEPVKAICKGIATSKN 56
QY 59 VLSTTRFQNLNCTRTSITPRPCPYSSRTETNYICVKCENQYPVHFAGIGRC 109
DB 57 VLTTFEYLSDC---NVTSPCKYKXKSTNTFCVTCENQAPVHFVGVGSC 104

Search completed: January 22, 2004, 12:06:24
Job time : 35.6067 secs